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(54) Title: NOVEL COMPOUNDS			
(57) Abstract <p>This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.</p>			

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the
5 production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

10 Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that
15 DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement
20 factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides
25 critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognized targets.

Brief Description of the Invention:

This invention provides novel proteins, particularly those from *Streptococcus*
30 *pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

10 It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

15 It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

20 In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

30 In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by
5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this
10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine
15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or
20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel *et al.*, Science 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

The basis of the technique is the random mutagenesis of target organism by various
30 means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In Streptococcus pneumoniae, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are
10 implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those
15 fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally
20 upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

3) Differential display

This technique is described by Chuang et al., J. Bacteriol. 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method
25 identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

This technique, described by de Lorenzo, V. *et al.*, Gene 123:17-24 (1993); Neuwald, A. F. *et al.*, Gene 125: 69-73(1993); and Takiff, H. E. *et al.*, J. Bacteriol. 174:1544-1553(1992), the contents of which is incorporated by reference for

5 background purposes, identifies genes whose expression are essential for cell viability.

In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which

10 separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the

15 absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.

20 **5) Generation of conditional lethal mutants by chemical mutagenesis.**

This technique is described by Beckwith, J., Methods in Enzymology 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent

25 replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene

30 allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute halflives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzol (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzol reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northernblots with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

Streptococcus pneumoniae, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same
5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring
10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only
15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a
polynucleotide which includes only coding sequence for the polypeptide as well as a
20 polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding
sequence for the mature polypeptide may be fused in the same reading frame to a
polynucleotide sequence which aids in expression and secretion of a polypeptide from a
host cell, for example, a leader sequence which functions as a secretory sequence for
25 controlling transport of a polypeptide from the cell. The polypeptide having a leader
sequence is a preprotein and may have the leader sequence cleaved by the host cell to form
the mature form of the polypeptide. The polynucleotides may also encode for a proprotein
which is the mature protein plus additional 5' amino acid residues. A mature protein having
a prosequence is a proprotein and may be an inactive form of the protein. Once the
30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a
mature protein, or for a protein having a prosequence or for a protein having both a
prosequence and a presequence (leader sequence). Further, the amino acid sequences
provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

The polynucleotides of the present invention may also have the coding sequence
5 fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Quiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.

10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides. As herein used, the term "stringent conditions"
15 means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization
20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*,
25 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the
30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match

5 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds.,

10 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity

15 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990). The BLAST X program is publicly available from NCBI and other sources (*BLAST*

20 *Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide

25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another

30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be
5 one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to the polypeptide, such as a leader or secretory sequence or a sequence which is employed for
10 purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

15 The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector
20 and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

25 In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

30 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

Suitable expression vectors include chromosomal, nonchromosomal and synthetic
5 DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction
10 endonuclease site(s) by procedures known in the art.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli*. *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression
15 of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as
20 dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control elements), so that the DNA sequence encoding the desired protein is transcribed into RNA
25 in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* *tac* promoter or the protein A gene (*spa*) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739; 30 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda P_R, P_L and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.

An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this
5 embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks,
10 pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

15 Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage λ (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), Ylp5
20 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

25 Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold
30 Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use
5 of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system
10 secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from
15 inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by
20 methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography
25 (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that
30 functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

10 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

15 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

25 Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, e.g., Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cott n et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

5 Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to used RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify and analyze mutations. These primers may be used for, among othe4r things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

15 The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured using any on of the methods well known in the art for the quantation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

20 In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

30 In accordance with yet a further aspect of the present invention, there is provided the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule
5 substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which
10 enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a
15 labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of a polypeptide of
20 the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or
25 polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay.
30 Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically

5 acceptable carrier.

In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

The polypeptide may be used as an antigen for vaccination of a host to produce
10 specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal
15 antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the polypeptides of the present invention can be
20 obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that
25 polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies
30 which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition, polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

The polypeptide, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, Nature, 256:495-497(1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., Immunology Today 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention.

Using the procedure of Kohler and Milstein (supra, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

The hybridomas are screened to select a cell line with high binding affinity and favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. *et al.*, Nature 348:552-554(1990), and Marks, J. *et al.*, Biotechnology 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, Nature 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., Science 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (*supra*, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. *et al.*, Science 246:1275-1281 (1989).

Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in Hiatt, A. *et al.*, Nature 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.*, Nature 321:522-525 (1986), or Tempest *et al.*, Biotechnology 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation' ; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

5 The humanised monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme
10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

The invention also relates to inhibitors identified thereby.

15 The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate
20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA, 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l. Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include
25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application
30 for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to human patients, it is expected that the daily dosage level of the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 $\mu\text{g/kg}$ of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 μg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 μl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 μg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily

used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) *Nucleic Acids Res.*, 8:4057.

5 "Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

10 "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, supra, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

15 **Example 1**

Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae*

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA
20 sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison *et al.*, J. Bacteriol. 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA
25 polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E.coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel *et al.*, Science 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by
30 Pearce *et al.*, Mol. Microbiol. 9:1037 (1993) which carries the *erm* gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, *inter alia*, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., Proc. Nat'l. Acad. Sci. USA 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of
 5 reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, eg., Swiss
 10 and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (J. Antimicrobiol. Chemother. 32:432 (1993) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6.
 15 Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as
 20 probes as described in Hensel et al., Science 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison et al., J. Bacteriol. 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies.
 25 Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a
 30 screen as described above.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each

ORF encodes more than one ORF. For example, SEQ ID NO:224 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:225 and 226 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the polynucleotide of SEQ ID NO: 2 encodes the ORFs of SEQ ID NOS: 225 and 226. Table 1 also shows the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF.

TABLE 1

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
224.	Phosphate Transport ATP-Binding Protein PSTB. - <i>Escherichia</i>	1	-CAT	TCA~	2	553	Reverse
225.	probable ATP binding protein - <i>Bacillus subtilis</i>	1	-CAT	TCA~	38	781	Reverse
226.	Nopaline Transport System Permease Protein Nocr. - <i>Agrobacterium Tumefaciens</i>	2	-CAG	TTA~	781	1512	Reverse
227.	Aspartate Aminotransferase A (EC 2.6.11) (Transaminase A) (ASPAT.) - <i>Rhizobium Meliloti</i> .	1	ATG	TAG	480	671	Forward
228.	ISL2 protein - <i>Lactobacillus helveticus</i>	1	ATG	TAA	549	947	Forward
229.	ISL2 protein - <i>Lactobacillus helveticus</i>	2	ATG	TAG	889	1353	Forward
230.	Unknown	3	ATG	TGA	1421	1570	Forward
231.	Unknown	2	-CAT	CTA~	111	413	Reverse
232.	Unknown	1	ATG	TGA	133	282	Forward
233.	Acyl Carrier Protein (ACP.) - <i>Rhizobium Meliloti</i> .	1	-CAT	CTA~	673	906	Reverse
234.	Unknown	1	-CAT	TTA~	15	137	Reverse
235.	Unknown	2	-CAT	CTA~	681	989	Reverse
236.	Sulfate Transport System Permease Protein CYST (Fragment). - <i>Synechocystis SP.</i> (Strain PCC 6803).	2	-CAT	TTA~	336	689	Reverse
237.	probable transposase (insertion sequence IS861) - <i>Streptococcus agalactiae</i> (strain COH-1)	2	-CAT	TCA~	149	454	Reverse
238.	Unknown	2	-CAG	TTA~	567	851	Reverse
239.	"PTS SYSTEM	1	ATG	TAA	49	477	Forward
240.	"PTS SYSTEM	2	-CAT	TTA~	151	789	Reverse
241.	nitrogen fixation protein (nifS) homolog - <i>Haemophilus influenzae</i> (strain Rd KW 20)	1	-CAT	TCA~	1	207	Reverse
242.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	1	-CAT	TCA~	84	431	Reverse
243.	surface protein PspA - <i>Streptococcus pneumoniae</i>	1	ATG	TAA	22	321	Forward
244.	Unknown	2	ATG	TAA	272	469	Forward
245.	ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - <i>Lactococcus lactis</i> subs p. lactis	1	ATG	TGA	83	760	Forward

	plasmid pUCL22						
246.	Beta-Glucosidase (EC3.2.1.21) (Gentiobiase) (Cellobiase)) (Beta-D-Glucoside GL Ucohydrolase) (Amygdalase). - <i>Bacillus Subtilis</i> .	1	-CAT	TCA-	153	599	Reverse
247.	Glycine Betaine/L-Proline Transport ATP - Binding Protein Prov. - <i>Escherichia Col. I.</i>	2	ATG	TAA	159	887	Forward
248.	Unknown	3	-CAT	TTA-	1102	1254	Reverse
249.	30S Ribosomal Protein S11 (BS11). - <i>Bacillus Subtilis</i> .	1	ATG	TGA	15	164	Forward
250.	DNA - Directed RNA Polymerase Alpha Chain (EC 2.7.7.6) (Transcriptase Alpha Chain). - <i>Bacillus Subtilis</i> .	2	ATG	TAA	282	1217	Forward
251.	Peptide Chain Release Factor 3 (RF-3). - <i>Bacteroides Nodosus</i> (<i>Dichelobacter Nod Osus</i>).	1	ATG	TAG	212	667	Forward
252.	Unknown	1	ATG	TAG	267	353	Forward
253.	Riboflavin Synthase Alpha Chain (EC 2.5.1.9). - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	213	662	Reverse
254.	Unknown	3	-CAT	TTA-	833	1045	Reverse
255.	Unknown	1	-CAT	TTA-	83	424	Reverse
256.	mesl protein - <i>Leuconostoc mesenteroides</i>	2	ATG	TAG	448	1302	Forward
257.	Transacetylase BMTD (EC 2.3.1.-). - <i>Bacillus Subtilis</i> .	1	CTG	TAG	3	320	Forward

			Cod n		Position		
SEQ ID NO:	Identity	ORF #	Start	Stop	Start	Stop	Direction
258.	ribose-phosphate pyrophosphokinase (EC 2.7.6.1.) - Bacillus caldolyticus	1	CTG	TAG	1	642	Forward
259.	Unknown	1	ATG	TAA	66	614	Forward
260.	Unknown	1	ATG	TAG	108	590	Forward
261.	nitrogenase C (nifC) homolog - Haemophilus influenzae (strain Rd KW20)	2	ATG	TAG	631	855	Forward
262.	Unkown	2	ATG	TAA	606	752	Forward
263.	Unknown	2	ATG	TGA	280	495	Forward
264.	Unknown	2	ATG	TGA	639	1466	Forward
265.	Acetyl Esterase (EC 3.1.-.-) - Caldocellum Saccharolyticum.	2	ATG	TAA	274	594	Forward
266.	Unknown	1	-CAT	TCA-	2	157	Reverse
267.	Triosephosphaste Isomerase (EC 5.3.1.1) (TIM). - Bacillus Subtilis.	1	-CAT	TTA-	270	665	Reverse
268.	Branched-chain Amino Acid Aminotransferase (EC 2.6.1.42) (Transaminase B). - ES Cherichia Coli.	1	ATG	TAG	110	736	Forward
269.	branched-chain-amino-acid transaminase homolog - Haemophilus influenzae (strain Rd KW20)	2	ATG	TAA	708	842	Forward
270.	DnaK protein - Lactococcus lactis	1	CTG	TGA	3	749	Forward
271.	Ketol-Acid Reductoisomerase (EC 1.1.1.86) (Acetohydroxy-Acid Isomeroreductase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis)	1	ATG	TAA	99	428	Forward
272.	Unknown	1	-CAT	CTA-	278	631	Reverse
273.	Amidophosphoribosyltransferase Precursor (EC 2.4.2.14) (Glutamine Phosphoribosy Lpyrophosphaste Amidotransferase) (Atase). - Bacillus Subtilis.	2	-CAT	CTA-	152	775	Reverse
274.	Pyrolidone-Carboxylate Peptidase (EC 3.4.19.3) (5-Oxopropyl-Peptidase). - STR Eptococcus Pyogenes.	1	-CAT	TCA-	156	803	Reverse
275.	50S Ribosomal Protein L16. - Mycoplasma Capricolum.	1	ATG	TAA	33	416	Forward
276.	serine O-acetyltransferase (EC 2.3.1.30) - Bacillus stearothermophilus	2	-CAT	CTA-	577	1194	Reverse
277.	Unknown	1	ATG	TAG	61	648	Forward

278.	Unknown	1	-CAT	CTA~	165	335	Reverse
279.	Lipoprotein Signal Peptidase (EC 3.4.23.36) (Prolipoprotein Signal Peptidase) (Signal Peptidase II) (Spase II). - Staphylococcus Aureus.	1	ATG	TAA	56	517	Forward
280.	Unknown	1	ATG	TAA	214	534	Forward
281.	Alpha-Acetolactate Decarboxylase (EC 4.1.1.5). - Bacillus Subtilis.	1	-CAT	CTA~	104	445	Reverse
282.	Dihydrodipicolinate Synthase 9EC 4.2.1.52) (DHDPS). - Bacillus Subtilis.	3	-CAT	TCA~	675	884	Reverse
283.	Polyribonucleotide Nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide Phosphorylase) (Pnpase). - Photobacterium Luminescens.	1	-CAT	TCA~	1	855	Reverse
284.	Single-Strand Binding Protein (SSB) (Helix-Destabilizing Protein). - Bacillus Subtilis	1	-CAT	TTA~	128	598	Reverse
285.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - Escherichia Coli.	2	-CAT	CTA~	195	482	Reverse
286.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - Escherichia Coli	4	-CAG	TCA~	676	990	Reverse
287.	N-(5'-Phosphoribosyl) Anthranilate Isomerase (EC 5.3.1.24) (PRAI). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	1	ATG	TAA	83	712	Forward
288.	30S Ribosomal Protein S2. - Escherichia Coli.	1	ATG	TGA	277	591	Forward
289.	30S Ribosomal Protein S2. - Escherichia Coli.	3	ATG	TGA	918	1064	Forward
290.	Possible beta-galactosidase precursor	1	-CAT	CTA~	120	545	Reverse
291.	Unknown	1	-CAT	TTA~	77	283	Reverse
292.	Unknown	1	-CAT	TTA~	1	198	Reverse
293.	"Phospho-2-Dehydro-3-Deoxyheptonate Aldolase	1	-CAT	TTA~	217	690	Reverse

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
294.	Unknown	2	-CAT	TTA~	429	599	Reverse
295.	Unknown	3	-CAT	TCA~	739	936	Reverse
296.	Sorbitol Dehydrogenase (EC 1.1.1.14) (L-Iditol 2-Dehydrogenase). - <i>Bacillus Subtilis</i> .	1	ATG	TAA	64	480	Forward
297.	EBG Operon Repressor. - <i>Escherichia Coli</i> .	2	-CAT	CTA~	668	1060	Reverse
298.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	2	-CAT	TTA~	249	566	Reverse
299.	Unknown	3	-CAT	TCA~	581	964	Reverse
300.	Adenylosuccinate Lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA~	99	809	Reverse
301.	ATP-Binding Protein BEXA. - <i>Haemophilus Influenzae</i> .	1	ATG	TGA	111	404	Forward
302.	L-Lactate Dehydrogenase (Cytochrome) (EC 1.1.2.3). - <i>Escherichia Coli</i> .	2	ATG	TAA	337	507	Forward
303.	Phosphate Transport System Permease Protein PSTC. - <i>Escherichia Coli</i> .	3	ATG	TGA	507	1070	Forward
304.	Sulfate Transport ATP-Binding Protein Cysa. - <i>Synechococcus SP. (Strain PCC 7942) (Anacystis Nidulans R2)</i> .	1	-CAT	CTA~	110	838	Reverse
305.	Unknown	2	-CAT	TTA~	838	1077	Reverse
306.	Unknown	2	-CAT	TCA~	282	749	Reverse
307.	Unknown	2	ATG	TAG	1108	1290	Forward
308.	Phosphoribosylformylglycinamide Cyclo-Ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-Aminoimidazole Synthetase) (AIR Synthase). - <i>Bacillus Subtilis</i> .	2	-CAT	TCA~	331	477	Reverse
309.	Unknown	2	ATG	TAA	313	765	Forward
310.	SMS Protein. - <i>Escherichia Coli</i> .	1	-CAT	TCA~	102	416	Reverse
311.	sigma 42 protein - <i>Enterococcus faecalis</i>	1	-CAT	TCA~	8	487	Reverse
312.	Unknown	1	-CAT	TTA~	76	390	Reverse
313.	Guanylate Kinase (EC 2.7.4.8) (GMP Kinase). - <i>Escherichia Coli</i> .	2	-CAG	TTA~	415	849	Reverse
314.	Unknown	1	-CAT	TCA~	51	296	Reverse
315.	Unknown	1	ATG	TAA	175	285	Forward
316.	Unknown	2	ATG	TAA	361	558	Forward
317.	Unknown	3	ATG	TAA	383	1144	Forward

318.	"PTS System	2	-CAT	TCA~	166	465	Reverse
319.	L-Fucose Isomerase (EC 5.3.1.-) - Escherichia Coli.	1	-CAT	CTA~	9	482	Reverse
320.	Unknown	2	-CAT	TTA~	495	650	Reverse
321.	Unknown	1	ATG	TGA	130	231	Forward
322.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli.	1	-CAT	TCA~	51	200	Reverse
323.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Car Rier Protein Reductase). - Escherichia Coli.	2	-CAT	TCA~	231	614	Reverse
324.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	1	-CAT	TTA~	31	231	Reverse
325.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	2	-CAT	TCA~	191	334	Reverse
326.	Unknown	3	-CAT	TCA~	309	452	Reverse
327.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A- IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	4	-CAT	TTA~	495	1127	Reverse
328.	Unknown	2	-CAT	TCA~	170	469	Reverse
329.	Unknown	1	ATG	TAG	105	473	Forward
330.	Strscaa Ncbi gi: 310629NCBI gi: 473 - Streptococcus gordonii (strain PK488) DNA	1	-CAG	CTA~	81	665	Reverse

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
331.	Unknown	1	ATG	TGA	228	374	Forward
332.	lysyl aminopeptidase (EC 3.4.11.15) precursor - <i>Lactococcus lactis</i>	1	-CAT	TCA~	107	766	Reverse
333.	Indole-3-Glycerol Phosphate Synthase (EC 4.1.1.48) (IGPS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	-CAT	TCA~	127	369	Reverse
334.	Anthranilate Phosphoribosyltransferase (EC 2.4.2.18).- <i>Lactococcus Lactis</i> (Sub SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	2	-CAA	TCA~	366	641	Reverse
335.	Tagatose-6-Phosphate Kinase (EC 2.7.1.-) (Phosphotagatokinase). - <i>Lactococcus L. Actis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	ATG	TGA	42	524	Forward
336.	Unknown	1	ATG	TGA	73	474	Forward
337.	Unknown	1	-CAT	TTA~	32	286	Reverse
338.	Unknown	1	ATG	TGA	306	572	Forward
339.	Acetolactate Synthase Large Subunit (EC 4.1.3.18) (AHAS) (Acetphydroxy-Acid Synthase Large Subunit) (ALS). - <i>Lactococcus Lactis</i> (SUBSP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	ATG	TAG	59	502	Forward
340.	Penicillin-Binding Proteins 1A/1B. - <i>Bacillus Subtilis</i> .	2	ATG	TGA	535	720	Forward
341.	Unknown	1	ATG	TAG	165	488	Forward
342.	Anthranilate Phosphoribosyltransferase (EC 2.4.2.18). - <i>Lactococcus Lactis</i> (SUB SP. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	-CAT	TCA~	5	394	Reverse
343.	grpE protein - <i>Lactococcus Lactis</i>	2	ATG	TAA	124	543	Forward
344.	Unknown	1	-CAT	CTA~	34	195	Reverse
345.	Unknown	2	-CAT	TTA~	377	544	Reverse
346.	Unknown	2	ATG	TAA	159	503	Forward
347.	Unknown	2	-CAT	CTA~	315	644	Reverse
348.	Unknown	2	-CAT	CTA~	468	587	Reverse
349.	Unknown	2	-CAT	CTA~	482	631	Reverse
350.	Unknown	2	-CAT	TTA~	380	757	Reverse
351.	NIFS Protein Homolog (Fragment). - <i>Lactobacillus Delbrueckii</i> (SUBSP. <i>Bulgaricus</i>).	1	ATG	TAG	87	797	Forward
352.	"Ornithine Carbamoyltransferase	1	TTG	TAA	2	502	Forward

353.	PSEGLI NCBI gi: 499660 - <i>Pseudomonas putida</i> .	1	-CAT	TTA~	50	481	Reverse
354.	Unknown	1	CTG	TAA	1	522	Forward
355.	Thioredoxin. - <i>Streptomyces Clavuligerus</i> .	1	ATG	TAG	58	375	Forward
356.	D-alanine permease (dagA) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	1	ATG	TAG	185	343	Forward
357.	Unknown	1	-CAT	TTA~	78	371	Reverse
358.	"DNA Polymerase III	1	-CAA	TCA~	82	561	Reverse
359.	Transport ATP-Binding Protein Coma. - <i>Streptococcus Pneumoniae</i> .	1	-CAT	TTA~	112	552	Reverse
360.	Unknown	2	ATG	TAA	445	540	Forward
361.	surface protein PspA - <i>Streptococcus pneumoniae</i>	1	-CAT	TCA~	45	416	Reverse
362.	Licid Protein. - <i>Haemophilus Influenzae</i>	2	ATG	TAA	268	633	Forward
363.	Unknown	2	ATG	TAA	527	640	Forward
364.	Glutamine Transport ATP- Binding Protein GLNQ. - <i>Escherichia Coli</i> .	1	CTG	TGA	1	393	Forward
365.	Unknown	1	ATG	TAG	184	303	Forward
366.	Unknown	1	ATG	TGA	794	919	Forward
367.	Lipoamide Dehydrogenase Component (E3) of Pyruvate Dehydrogenase Complex (EC 1.8.1.4) (Dihydrolipoamide Dehydrogenase). - <i>Azotobacter Vinelandii</i> .	1	ATG	TAA	3	416	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
368.	Orotate Phosphoribosyltransferase (EC 2.4.2.10) (OPRT). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA~	21	311	Reverse
369.	Unknown	1	ATG	TAA	28	309	Forward
370.	SPO0B-Associated GTP-Binding Protein. - <i>Bacillus Subtilis</i> .	1	ATG	TGA	110	538	Forward
371.	Transport ATP-Binding Protein COMA. - <i>Streptococcus Pneumoniae</i> .	1	-CAA	TCA~	47	679	Reverse
372.	prephenate dehydrogenase (EC 1.3.1.12) - <i>Lactococcus lactis</i> .	2	ATG	TAG	271	492	Forward
373.	O-Sialoglycoprotein Endopeptidase (EC 3.4.24.57) (Glycoprotease). - <i>Pasteurella Haemolytica</i> .	1	CTG	TAA	1	450	Forward
374.	Unknown	1	-CAT	TTA~	7	282	Reverse
375.	Unknown	1	TTG	TAA	2	265	Forward
376.	"DNA Polymerase III	1	ATG	TGA	3	401	Forward
377.	Unknown	2	ATG	TAA	361	516	Forward
378.	Dihydrodipicolinate Synthase (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA~	179	457	Reverse
379.	Unknown	2	-CAT	TCA~	104	322	Reverse
380.	Unknown	2	-CAT	TCA~	248	649	Reverse
381.	Unknown	1	-CAT	TTA~	56	394	Reverse
382.	Unknown	2	-CAT	TTA~	254	409	Reverse
383.	Unknown	1	ATG	TAG	138	617	Forward
384.	Unknown	2	-CAT	TTA~	225	479	Reverse
385.	Unknown	2	ATG	TAA	747	857	Forward
386.	Unknown	1	ATG	TAG	294	443	Forward
387.	Unknown	2	ATG	TGA	356	544	Forward
388.	Unknown	1	-CAT	CTA~	4	141	Reverse
389.	Unknown	1	CTG	TAG	1	579	Forward
390.	Unknown	2	-CAT	TTA~	309	452	Reverse
391.	Phosphopentomutase (EC 5.4.2.7). - <i>Escherichia Coli</i> .	1	ATG	TAA	3	233	Forward
392.	D-Alanyl-D-Alanine Carboxypeptidase Precursor (EC 3.4.16.4) (DD-Peptidase)(DD - Carboxypeptidase)(Cpase)(PBP5). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA~	52	537	Reverse
393.	Na+ and Cl-dependent gamma-aminobutyric acid transporter homolog- <i>Haemophilus</i>	1	TTG	TGA	2	268	Forward

	influenzae (strain Rd KW20)						
394.	Unknown	2	ATG	TGA	319	546	Forward
395.	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Pelobacter carbinolicus	1	ATG	TGA	3	284	Forward
396.	Unknown	2	ATG	TGA	241	450	Forward
397.	Beta-Glucosidase A (EC 3.2.1.21)(Gentiobiase)(Cellobiase)(Beta-D-Glucoside Glucohydrolase). - Clostridium Thermocellum.	1	ATG	TAA	184	453	Forward
398.	Uracil Permease. - Bacillus Caldolyticus.	1	ATG	TAA	93	353	Forward
399.	Unknown	2	ATG	TAG	127	516	Forward
400.	ligoendopeptidase F- Lactococcus lactis	1	ATG	TGA	134	310	Forward
401.	Stratpasea NCBI gi: 153565NCBI gi: 4- Streptococcus Faecalis DNA.	2	ATG	TAA	392	568	Forward
402.	Unknown	2	ATG	TAA	376	507	Forward
403.	Exodeoxyribonuclease Small Subunit (EC 3.1.11.6) (Exonuclease VII Small Subunit). - Escherichia Coli.	2	-CAT	TCA-	470	682	Reverse
404.	ATP-Depenent DNA Helicase RECG (EC 3.6.1.-). - Escherichia Coli.	1	ATG	TGA	3	455	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
405.	Possible thiamin biosynthetic enzyme	1	-CAT	TTA~	15	347	Reverse
406.	SPOU Protein. - Escherichia Coli.	2	ATG	TAA	322	618	Forward
407.	Malonyl Coa-Acyl Carrier Protein Transacylase (EC 2.3.1.39). - Escherichia Coli.	1	ATG	TAG	85	498	Forward
408.	Unknown	1	-CAT	CTA~	17	118	Reverse
409.	nucleoside diphosphate kinase (ndk) homolog- Haemophilus influenzae (strain Rd KW20)	1	CTG	TGA	1	159	Forward
410.	Nucleoside Diphosphate Kinase (EC 2.7.4.6)(NDK) (NDP Kinase). - Escherichia Co LI.	2	ATG	TAG	215	481	Forward
411.	Unknown	1	-CAT	TTA~	21	368	Reverse
412.	Unknown	2	-CAT	TCA~	162	314	Reverse
413.	Unknown	1	ATG	TAA	187	417	Forward
414.	Unknown	2	ATG	TGA	316	417	Forward
415.	Unknown	1	ATG	TGA	316	453	Forward
416.	Enolase (EC 4.2.1.11)(2-Phosphoglycerate Dehydratase)(2-Phospho-DOGlycerate Hydro-Lvase). - Bacillus Subtilis.	1	-CAT	TTA~	4	435	Reverse
417.	Unknown	1	CTG	TGA	1	363	Forward
418.	Unknown	1	ATG	TGA	39	383	Forward
419.	PILB Protein. - Neisseria Gonorrhoeae.	1	-CAT	TTA~	145	327	Reverse
420.	Unknown	2	ATG	TGA	285	533	Forward
421.	Unknown	1	CTG	TAG	2	379	Forward
422.	integrase/recombinase (xprB) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAA	305	421	Forward
423.	Unknown	1	-CAT	CTA~	173	436	Reverse
424.	Unknown	1	-CAT	CTA~	182	427	Reverse
425.	Unknown	1	ATG	TAA	49	372	Forward
426.	"Mutator Mutt Protein (7	1	-CAT	CTA~	21	446	Reverse
427.	Unknown	1	ATG	TGA	177	380	Forward
428.	Possible phosphatase	1	ATG	TAG	112	402	Forward
429.	Unknown	1	ATG	TGA	110	271	Forward
430.	Phosphoenolpyruvate Carboxylase (EC 4.1.1.31). - Corynebacterium Glutamicum.	2	ATG	TGA	337	561	Forward
431.	Unknown	1	ATG	TGA	214	324	Forward
432.	50S Ribosomal Protein L31. - Bacillus	1	ATG	TAA	142	426	Forward

	Subtilis.						
433.	glycosyl transferase (lgtD) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TGA	127	399	Forward
434.	Unknown	2	-CAT	CTA~	244	435	Reverse
435.	Unknown	2	ATG	TGA	118	309	Forward
436.	Factor essential for Expression of Methicillin Resistance. - Staphylococcus Aur Eus.	2	-CAT	TTA~	168	434	Reverse
437.	Unknown	1	-CAT	TCA~	2	214	Reverse
438.	Unknown	1	TTG	TAA	2	142	Forward
439.	Unknown	1	ATG	TAA	30	191	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
440.	Aspartate Aminotransferase (EC 2.6.1.1) (Transaminase A)(ASPAT). - Bacillus SP. (STRAIN YM-2).	1	-CAT	TCA~	63	416	Reverse
441.	Unknown	1	ATG	TAA	52	342	Forward
442.	Unknown	2	-CAT	TCA~	210	455	Reverse
443.	Unknown	1	TTG	TGA	2	517	Forward
444.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-) - Escherichia Coli.	1	ATG	TGA	83	376	Forward
445.	Unknown	1	ATG	TAA	70	384	Forward
446.	Cell Division Protein FTSA. - Bacillus Subtilis.	1	TTG	TAA	3	371	Forward
447.	Unknown	1	ATG	TAG	70	441	Forward
448.	Unknown	1	ATG	TAG	104	454	Forward
449.	Unknown	1	CTG	TAA	1	159	Forward
450.	Unknown	1	ATG	TAA	120	347	Forward
451.	Unknown	1	ATG	TGA	31	423	Forward
452.	Unknown	2	ATG	TGA	225	416	Forward
453.	Unknown	1	ATG	TGA	290	418	Forward
454.	Unknown	1	ATG	TGA	3	269	Forward
455.	JAG Protein (SPOIIIJ Associated Protein). - Bacillus Subtilis.	1	ATG	TGA	93	365	Forward
456.	"DNA -3-Methyladenine Glycosidase I (EC 3.2.2.20)(3-Methyladenine-DNA Glycosylase I	1	ATG	TAG	91	282	Forward
457.	"Glucan I	1	-CAT	TTA~	4	150	Reverse
458.	Unknown	1	-CAT	CTA~	245	400	Reverse
459.	Glutamate/Aspartate Transport ATP-Binding Protein GLTL. - Escherichia Coli.	1	-CAT	TCA~	81	218	Reverse
460.	Unknown	1	-CAT	TTA~	103	492	Reverse
461.	Unknown	1	ATG	TGA	305	484	Forward
462.	Unknown	1	-CAT	TCA~	29	355	Reverse
463.	Unknown	2	-CAT	TTA~	572	838	Reverse
464.	Unknown	2	-CAT	TCA~	652	1026	Reverse
465.	Unknown	2	-CAT	TTA~	318	764	Reverse
466.	Unknown	2	ATG	TGA	719	805	Forward
467.	Llcpyrda NCBI gi: 511014 - Lactococcus lactis.	1	ATG	TGA	134	472	Forward

468.	Unknown	1	ATG	TGA	385	492	Forward
469.	Unknown	2	ATG	TAA	587	721	Forward
470.	galE protein - Neisseria meningitidis	1	-CAT	TCA-	23	460	Reverse
471.	Unknown	2	-CAG	TTA-	717	1319	Reverse
472.	Naphthoate Synthase (EC 4.1.3.36) (Dihydroxynaphthoic Acid Synthetase)(Dhna Sy Nthetase). - Escherichia Coli.	1	ATG	TGA	97	414	Forward

				Cod n		Position		
SEQ ID NO:	Identity	ORF #	Start	Stop	Start	Stop	Direction	
473.	Unknown	1	CTG	TGA	1	246	Forward	
474.	Unknown	1	-CAT	TCA-	341	748	Reverse	
475.	Unknown	1	-CAT	TTA-	217	858	Reverse	
476.	Unknown	1	-CAT	TTA-	499	729	Reverse	
477.	Multiple Sugar-Binding Transport ATP-Binding Protein MSMK. - Streptococcus MUTA NS.	2	ATG	TAA	407	571	Forward	

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:224. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:225 and SEQ ID NO:226.

TABLE 2

DNA	Protein (open reading frame)
===	=====
1	224
2	225,226
3	227
4	228,229,230
5	231
6	232
7	233
8	234
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12	238
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17	243,244
18	245
19	246
20	247,248
21	249,250
22	251
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24	253,254
25	255,256
26	257
27	258
28	259
29	260,261
30	262

31	263
32	264
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34	266
35	267
36	268,269
37	270
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52	285,286
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54	288,289
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64	302,303
65	304,305
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71	311
72	312,313

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79	324,325,326,327
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84	332
85	333,334
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94	343
95	344,345
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211	462,463
212	464
213	465
214	466
215	467
216	468,469
217	470,471
218	472
219	473
220	474
221	475
222	476
223	477

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Black, Michael
Hodgson, John
Knowles, David
Nicholas, Richard
Stodola, Robert

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 01-APR-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014690
(B) FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/025788
(B) FILING DATE: 22-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891

(C) REFERENCE/DOCKET NUMBER: P50466

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAACATG GTCTCTTCTA GTTGCATGGT CGCAATCGGA TCCAAGGCTG AGGCTGGGCT	60
CATCCATTAA GAGGATATCT GGCTTAACAG AGATGGCAGC AGCGATACAG AGACGTTGTT	120
GCTGACCACC TGATAAGGTC AAGGCTGACT TGTGGAGATC GTCTTTAACC TGATCCCCAA	180
GGGCAGCCTG ACTAAGGGAG GTTTCTACGA TTTTCATCTAG GACTTGCTTA TCCTTAACTC	240
CAGCACGTTT ATGCGCAAAG GTAATATTAC GGTAAATTGA CTTAGCAAAT GGATTGGGGC	300
GTTGAAAAAC CATTCCAATG TGTTTACGCA TTTCATAAAC GTTGATTTCT GGACGGTTGA	360
CATCAATTCC ACGATAGAGA ATCTGCCCAG TTACTTTAGC AATATCAATG GTATCATTCA	420
TGCGATTGAG ACTGCGTAAG TAGGTAGATT TCCCCGATCC CGACGGACCA ATCAAAGCTG	480
TAATTTTATT TCCTTTCAA TTGCATATCA ATCCCCTTAA TGGATTCATT TTTACCATAG	540
TAAACATGGA CATCCTTAGT AGAAAGGGCT ACTTTTCTT CAGGAAAGGT AAGGATATGC	600
TTCTCATCCC AGTTATATGT TGACATGGCT TCTCCTTTAG GCAGCGGTTA ATTTCTTGTC	660
TAGATAGCTT CCGAACTTAC GAG	683

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGTCCAAC	TAAGTGAAGT	TTCCTTTATC	TATTATATCA	AATATAAGTC	CGTTTGTAAC	60
TAGTGAAGAA	TTCTTTTGTC	CGCTCTTCTT	TAGGGGTGTG	GATAATCTCA	TCCGGAGTTC	120
CAGACTCGAT	GATTTTCCCC	TTATCTAAGA	AGAGAATTTT	ATCCGCAACT	TGGGCTACAA	180
AGGGCATGTC	ATGACTGACC	AAAATCATGG	TCTGACCTGA	CTTAGCAGCA	TCTGCAATAG	240
ACTTTTCTAC	TTCACCGACC	AATTCTGGGT	CAAGGGCTGA	AGTTGGTTTCG	TCTAAGAGCA	300
AAACATCTGG	TTTCATAGCA	AGCGCACGCG	CTAGGGCAAC	CCGTTGCTTC	TGTCCACCTG	360
ATAAATGGCG	AGGATAATGG	TTTTCACGGT	CCGAAAGCCC	AACCTTAGCC	AACTCTTCCT	420
TGGCAATCTT	AGTCGCTTCT	TGGTCAGATA	ATTCTTGAC	AACAACCAAG	CCTTCTTTCA	480
CATTATCAAG	TGCTGTTCCG	CGTTCAAATA	AATTAAACTG	TTGGAAAACC	ATAGACAACT	540
TACGGCGTAG	GGCAAGGATT	TCTTCTTGAG	TGATTTTAGA	AAAATCAACT	GAAAAACCAT	600
CAATCTGAAT	AGAGCCACTG	TCAGGTGTTT	CAAGATAATT	GAGACTGCGA	AGAAAGGTTG	660
ATTTTCCAGC	TCCTGAAGAA	CCAATCAAGG	CTACAACCTC	CCCTTTTGA	ATATCCAAGT	720
TCAGATGATC	CAAGACAGTC	TGTCCTGAAA	AGGATTTGCT	TAAATTCGAA	ATCTTAATCA	780
TTAACGAAGG	TCTCCTTTCA	CATCTGTTTG	CACGTGATCA	GGTGCAGAAA	TAGCCATTTT	840
TCTCTCGATG	AAACGACCGA	GGCTTTCAAT	TCCGATATTG	ACTACCCAAT	AAACAAGGGC	900
AACAGAGATG	AAGCGTTCAA	AATAGCGATA	ATCAGCTCCA	CCTAGAATCT	GAGCTTGGGC	960
AAAGACTTCC	ACAACACCCG	CACTAAAAGC	TAGAGATGTT	CCCTTGGTCA	AACCGATGAG	1020
GGAATTAATC	AAGGTTGGAG	TAGCTACCAC	CGCTGCATTA	GGAATAATCA	CTCGTCGATA	1080
AACTTGCGCT	CGGGTCATAC	CCAGACTGCG	CGCCGCCTCA	ATCTCACCAG	GATTAACCTGA	1140
GAGAATGGCT	GCACGAATGG	TTTCACTAGC	ATAAGCTGCC	TCATTAAAGG	CAAAAGCGAC	1200
AATCGCAAAA	GCTGCAGCTG	GAATCGCATT	GATATTGAGA	CCAGTTCCCC	ATTGCTGATT	1260
GAGGGCTTTC	AAAGCCAAAG	GGATTCCGTA	GTAGGTCAAC	ATGAGTTGCA	CCAAAATCGG	1320
TGTCCCTTTT	AAGAACTAA	CAAAGAAGGC	CTGCAAGGGA	TATAAAATCT	TGACACGATT	1380
GATCTTCACA	ATGGCAAAAA	GAAGCGCCAA	AACCAAGCCA	AAAAGGGCAC	CGCCAATTGT	1440
CAACATAATT	GTTGTTGGAA	GTTGTTGGAC	AATTCTAGGG	ATTCCATCAA	AGACCGAACG	1500
TAGGCTAAAC	AG					1512

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGAGATTA	TTGAGATTGC	CCGTCAAAAC	GATTTGATTA	TNNTTGC	GGA	TGAAATCTAT	60
GACCGCATGG	TAAATGGACG	GACATGTGCA	TAACGCCTGT	GGCGAGCTTG	GCACCAGATG		120
TCTTCTGTGT	CAGCATGAAT	GGTCTGTCAA	AATCCCACCG	CATAGCAGGT	TTCCCGTGTG		180
GGATGGATGG	TCTTGTCTGG	CCCTAAGACT	CATGTTAAGG	GCTATATCGA	AGGGCTCAAT		240

ATGCTGTCCA ATATGCGCCT TTGCTCTAAC GTTTTGGCTA CCAACGCTGC ATTAGGAATA	300
ATCACTGTCTG TACAAACTTG CGCTTGGGGG GTCACCAATC AGTCGATGAA TTGCTTCTTC	360
CTGGTGGACG AATCTACGAG CAAAGAAATT TCATCTATAA TGCCATTCAA GATATTCCAG	420
GTTTGTCTGC CGTTAAACCC AAGGCGGGGC TCTATATCTT CCAAAAATC GACCGCAATA	480
TGTACCGTAT CGATGATGAT GAGCAGTTTG TCCTTGATTT CTTGAAGCAG GAAAAGGTTC	540
TCTTGGTTCA TGGTCGAGGC TTAACTGGC AGGAACCAGA CCACTCCGT ATCGTTTACC	600
TTCTCGTGT TGATGAGTTA GCCCAAATCC AAGAAAAGAT GACTCGTTTC TTGAAACAGT	660
ATCGTAGATA GGGCTTGCAT TCGAAAAAGC TGGAAACATT TGCCTAGAG	709

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGCTTCAGA ACCTGCCAAA CCAGCACCGA TAACATTGAT ATAAGATTGA GACACGACAC	60
TAATACCTCT TTGGGAGTGT GAAGTTAAGA TTCACATTGA AAAAGCCAAT CAGACTTACA	120
AGCTTTCGAG TTTCTTGGCT CAGGCTGAAA AAGTCCACAG GGCTTTTNCA CTCCCACAAA	180
TCTTTCTATT TTTTCTNCTA CTAGTATAAC AAAAAAGGG AAGAAGNAA ACTTCCCTGT	240
TTAGTCATTT TCTTGATGTA AAGAGATAGT GAGTATTCCA GTTAAGAATC AATTATATGC	300
TACTCTATAA AATCTTTTCC ACATAACGGA TCGATAGGGA CTGTTATTCT ATCTCTTGCT	360
ATAACCGTAT TATCTAAAAC AGCATAACAT TCAACATAGT GATCTCCTTT AAAGTGTGAA	420
TCTTCCGTGA TATTTTATTT TACCTGAAAA AATAGCACAC GCTCACAATT CTTCTAATA	480
GCCTCAGCTT CAATATTTCT TACTTTCCAA TAGACTCCCT GCGAAACAAA ATATGGTATA	540
GTAGTTCTAT GAATGATGAA GCAAGTAAAC AACTAACTGA TGCACGATTT AAGCGTCTTG	600
TTGGTGTTCA GCGCAGCACT TTTGAAGAGA TATTAGCTGT ATTAAAAACA GCTTATCAAC	660
TTAAACACGC AAAAGGTGGA CGAAAACTA AATTAAGCCT AGAAGACCTT CTTATGGCCA	720
CTCTTCAATA TGTGCGAGAA TATCGAACTT ATGAACAAAT TGCGGCTGAT TTTGGTATCC	780
ACGAAAGCAA CTTAATCCGT CGGAGCCAAT GGGTTGAAGT AACTCTTGTT CAAAGTGGTG	840
TTACGATTTT AAGAACTCCT CTCAGTTCTG AGGACACGGT AATGATTGAT GCGACGGAAG	900
TACAAATCAA TCGCCCTAAA AAAAGAATTA GCGAATCATT CTGGTAAAAA GAAATTTTAC	960
GCTATGAAGG CTCAAGCGAT TGTCACAAGT CAAGGGAGAA TTGTTTCTTT GGATATCGCT	1020
GTGAAGTATA GTCATGATAT GAAGTTGTTT AAAATGAGTT GCAGAAATAT CGGACAAGCT	1080
GGAAAAATCT TGGCTGATAG TGGTTATCAA GGGCCCATGA AGATATATCC TCAAGCACAA	1140
ACTCCACGTA AATCCAGCAA ACTCAAGCCG CTAATAGCTG AAGATAAAGC TTATAACCAT	1200
GCGCTATCCA AGGAGAGAAG CAAGGTTGAG AACATCTTTG CCAAAGTAAA AACGTTTAAA	1260
ATGTTTTCOA CAACCTATCG AAATCATCGT AAACGCTTCG GATTACGAAT GAATTTGATT	1320
GCTGGCATTG TCAATTATGA ACTAGGATTC TAGTTTTGCA GGAAGTCTAT TATTTTCTTT	1380

ATTGTCTGTA AGTCTACTGA CCTTGTTGTT TATCCCAGTC ATGGTTTCTA GTTCGGGGCTC	1440
AGAGTTTCAA AGTGGATGGC AAGAGCATCA ATTGATTGCT GAGAAGGTTA GTAAAACACT	1500
TGACAAGACA TTTGATAAGG ATGTCAGAAA AATCCGACC AGTCCAGTTT TATCAAAAAT	1560
TTGTAGATGA GATGGGAAGG ATTTACTC	1588

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTTTAA TACAGCTAAC ATCTCTTCAA AAGTGGTACG CTGAACACCA ACAAGACGCT	60
TAAATCGTGC ATCAGTTAGT TGTTTACTTG CTTCATCATT CATAGAACTA CTATACCATA	120
TTTTGTTTCG CAGGGAGTCT AATATTGTCA AATACTGGAG CGCTCATTGC TGGTATACGG	180
AATAAGATTG GCCCAGCTTC GATAACTGGG ATACCTGGTT CAAAACCAAG ATCTGTTGCA	240
GCGATTGGTG TAAAGATATC GTAACCTTTC ATAAGGTCTT CGTTTACATC TTTCACCATG	300
ACTGCATCAC AGTGAACATC ATAACCACGG TTTGAAAGTT CTTCTTCTAG AGCACTTTTA	360
ATTTGGTGAC TTGAGTTAAC ACCTGCACCG CAGGCAGCAA GAATTTTAAT CATTTAGATT	420
TCCTCCGATT TTATTTTTTA ATAGACAAGA TTAAGCGGTT GCTTCAGCAA TGTAAGCATA	480
AAGTTTTTCT GGTTCGGAAA TTTTGTATAG GTCTTCAAGA TGCCATTTC CTGTGAAAAA	540
GTCCATCAAC TGAGCCAGAA TATTTGTTTG ACTTGAACCT GAGTTATTGA TGATAAAGAA	600
GAGCAAGGAT ACTTCTACTT CCTTATCAGG AGCTATCATA TTGTGAAAAG TTAGTGATTT	660
TTCTAATCGA ACAACCACCA CTTTCTCAG	690

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTGCTACCT TTAAGAAGAT AGTAGACGTA TATACTTTTT TAAGAAAATC AAAAAGATAC	60
TATAAAAAAT CTATTTGTTT ATTGAATTTA AGACTTTGGT AACAAATTGA AAATAAAAAG	120

GAGGTATTCA TCATGAATAC AAAAATGATG TCACAATTTT CTGTTATGGA TAATGAAATG	180
CTTGCTTGCG TTGAAGGTGG AGATATTGAT TGGGGAAGAG AAATTAGTTG TGCAGCAGGG	240
GTTGCATATG GCGCAATTGA TGGGTGTGCA ACAACGGTTT GATATTTCTA TTGGGACCAT	300
TTGCTATAGG AATAGGTGTA ACTGGTGCTG CAGGTGGAG	339

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGAAGACCT CGTGCTACTC CTCCTCCAAC ACCTGCTTTG GCAAAATCTC CCCAATTGCA	60
TCCGCCACCT TCAACTCAAG CAAGCATCTC AGTATCCATA ATTTCAAATT GTGACATCTT	120
TTTGTATTTC ATAACGAATA CCTCTTTTTT ATTTTAAATA TTTGTCTTGT TACAAACTTG	180
ACAAGTTTAG TATAACAGTA TCTATTAATT TTTTTCATCC AAATCTTGAA TTGGCATCGA	240
AACGTCTTGA ATTAGCTTTT TTGTTTCAAA ATCATCTCTA TTTTAAAAA AGATGTTTTC	300
TAATCACTTT TTTACTATTT AGACTTCCTG CAAAAGTAGA ATCCTAGTTC ATGATTGATA	360
ATACCAGCAA TCAAATTCAT TCGTAATCCG AAGCGTTTAC GATGATTTCG ATAGGTTGTT	420
GAAAACATTT TAAACGTTTT TACTTTGGCA AAGATATTCT CAACCTTGCT TCTCTCCTTA	480
GATAGCGCAT GATTACAGGC TTTATCTTCA ACTGTTAGCG GCTTGAGTTT GCTGGATTTA	540
CGTGGAAGTT TGTGCTTGAG GATATATCTT CATGAGCCCT TGATAACCAC TGTCAGCCAA	600
GATTTTACCA GCTTGTCCGA TATTTCTCAT TTCTAAAAAC CATCTACTTC CGTTGACTTG	660
GAAGTCCGAT TGCTATTTTC CTTGAATGAT TTAAACCACA TCTCCTACAC TTTGGAGTTG	720
GTCAATTTCC TCATCGCTGA TTTGATACT AAATTCATCC TCCAGCGTCA AGATAAACTC	780
CATCAAATCA ACTGAGTCAG CATCCAAGTC GTCTTTCAGA CTCAAGGATT CTGTCACGAC	840
AAAGTCTCTT CCCTGTCGCT CTTGGATAAT GGTCAACAATA CTGTCAAAAA TTTCTTTTTT	900
TCTCATCTCT TTTATTTCTC TGAAAATTCA CGCGCAGTCT GGGCAACTAC TTCTGTTTCT	960
AGCATGGTAC GAATCTGGCG AATCGTACTA TAAACAGCCT TGGCATCGCT TGAGCCATGA	1020
GTCTTGACAA CAGGTGCCTT GACACCAAAC AAGACCGCTC CACCAACATC TGAATAATTG	1080
AGCTGTTTTT TCAAACCTCT GAGGCTGTCC TTGAGAAGGA GGGCACCTAG TTTGCTCGA	1140
AGACCACCAC CTGTAATAGC TGTCTTGAGC AAGCCCATGA TTCCCATAGC TGTCCCTTCG	1200
ATGGATTTGA GCACAGCGTT TCCCGTGAAA CCATCTGCCA CAACAACATC TGCAACGCCA	1260
TTTCATCAAT CACGCGCTTC CACGTTTCCG ATAAAGTTCA AACTTTTCATC AGCCGCCAGT	1320
AATTCATAAG TTTCTTACG AAGCGGGTCG CCCTTGCTAC TCTCTGTTCC GTTGTGAGC	1380
AAACCAACAC GTGGTTGCGC AATGCCACGA ACATTCTTGG CATAGAAAGA ACCTAGGACA	1440
GCGTATTGAT GGAGGTGCTG GGCTGTATTT TCTGCATTAG CACCGAGGTC AAGCATGTCA	1500
AAACCTTTCC CATCTACAGT CGGCAATGTT GACATAAGTC CAGGACGGTC GATATTCTTG	1560
ATACGACCCA CGATGAAGAA TCCAGCAGCC AACAAAGCAC CTGTATTCCC AGCCGAAAGG	1620

ACAGCGTCTG CTTCAACCATC TTTGACAGCC TTGGCTGCCA ATACCATACT GGCATTTTTTC 1680
TTATTCCGAA TAG 1693

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAATCTGC TTGCTTAGTC CACTTGCTTG AGCCAAGGAG TCACATACTC AAAATTTTCA 60
TGAAAGTCAT AGGTACCGTC TTCTTTTTTA GCTGAAAAGA AAAGTCCATC GTGGTAGAGC 120
AAATCCCCGT GGGCCATAAT TCTGGCAGTT TTTTCTCTT CCTACTCCTG AGACTTTTGC 180
TTAGTCCCCT CTTGAGAAAT AGTATCTCGT TTTTGACTAG TCAAGGGATT CCTTGGAAGC 240
TTTCAAACAA CAAGACCAAG CCCATTGATA AACCAACTGC TAGCAAGAGT ATCGCCACAA 300
ATCCCTTATT GCTCCACTTG CGATAACTCC TAAAAAGTTT ACCAAGCCCT TCATAAAACG 360
AAAAGCTAAA CCACCCTGAT TTCGATTTTG TCTTCTTTGT ATCTTCGTTC TCCCTACTTT 420
CTTATGCAAG CCTTTTCTTT TTATTATATC ACAGATAAGT ATTTCTTTCA CAATTGAATT 480
GAACTTCCCA TCTATTTTCT ATAAATCCTA AATGCCATAA TGCTTTCAAT TCCTGTCAAT 540
TTGTGATATC ATGTAGAAGA AATGAACTAA TCCACAGTGG CTTATTCCAA GTATACCACT 600
TGGGCTTTGG CAGTAG 616

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAATATAGA ATAATCACCG CCGTTGTGAA AGAACGATTG GATGATAATC CAATCGTTCA 60
GGGAAATTGG AAGACCTTGG GTTTCCAATT TAGGCATGAG ACACCTTTGG TGGCTGCTGC 120
CGTCCCTCAC AAGCTAAGGT GATTGTTGAA AAAGAGGAAA AAGGAGAAGA AATGAAACCA 180
GTAATTTCCA TCATCATGGG CTCAAATCC GACTGGGCAA CCATGCAAAA AACAGCAGAA 240
GTCCTAGACC GCTTCGGTGT AGCCTACGAA AAGAAAGTTG TTTCCGCACA CCGTACACCA 300

GACCTCATGT TCAAACATGC AGAAGAAGCC CGTAGTCGTG GCATCAAGAT CATCATCGCA	360
GGTGCTGGTG GCGCAGCGCA TTTGCCAGGC ATGGTAGCTG CCAAAACAAC CCTTCCAGTC	420
ATTGGTGTGC CAGTCAAGTC TCGTGCTCTT AGTGGAGTGG ATTCACCTCTA TTCTATCGTT	480
CAGATGCCGG GTGGGGTGCC TGTGCGACC ATGGCTATCG GTGAACTCTT TTTTAGGATA	540
TAAAACAGGG TTCGGATAAG TTTTTTTGCA AGGTGGATGA TGGCTACATT GTAATGTTTT	600
CCTTATTCTA ACTTAGTCTT AAGATAGGTC TTAAAACCAG GTGAAAAGCG AAGGCATGCT	660
TTGGCAGCTT GTATGAGTAC CTACCGCAGA TGAAGGGAAC CCCGTTTGAC CATCCTTCCA	720
ACTAAATCAA TCTGACCTGA CTGATAAATA GAAGAATCCA GTCCAGCGAA AGCTTGTAAT	780
TGAGCAGGAT TATCAAAGGC ATGAATATTT CGAATCTCGG CTAAATGAC CGCCCCATAA	840
CGATTCTCAA TCCCAGTAAC CGTCGTGATG ACCGAGTTTA ACTCAGCCAT CAAGTCATTG	900
ACACATTTTT CCGCCTTGTC AATGAGCCTC TTGTAATGTT TGATGTTTTT ATTACACGAG	960
ATAAACGTC TATGCGTTAT CAAACTCATT ACCAATTAAA ACAAATGTGG TTAGATCCTT	1020
TCGGAAATTG TCAAGCGATT GGAGGAAATG AACTAATCCA CAGCGGCTTA TTCCAAGTAT	1080
ACCACTTGGG CTTTGGCAGT AGCTAACTGC GCTAAATATA ATATAAGGAG GAGTAAAATG	1140
AAGACAGTTC AATTTTTTTG GCATTATTTT AAGGTCTACA AGTTCTCATT TGTAAGTGTC	1200
ATCCTGATGA TTGTTCTGGC GACTTTTGCC CAAGCCCTCT TTCCAGTCTA TTCTGGACAA	1260
GCGGTGACGC AGCTAGCCAA TTTAGTTCAA GCTTATCAAA ATGGGCAATC CAGAACTTGT	1320
ATGGCAAAGC CTATCAGGAA TTCATGGTCA ATCTTGGCCT GCTGGTTTTG GGTCTATTT	1380
ATCTCTAGGT GTAATATAAA CATGTGTCTC ATGACGCGCG TGATTGCAGA ATCGACCAAC	1440
GAGATGCGCA AAGGTCTCTT TGGTAAGCTT GCTCAGTTGA CGGTTTCTTT CTTTGACCGT	1500
CGACAAGATG GCGATATCCT GTCTCATTTT ACCAGTGATT TGGATAATAT CCTCCAAGCC	1560
TTTAACGAAA GCTTGATTCA GGTCATGAGC AATATTGTTT TATACATTGG TCTGATTCTT	1620
GTCATGTTTT CGAGAAATGT GACGCTGGCT CTCATCACCA TTGCCAGCAC CCCATTGGCT	1680
TTCTTTATGC TGATTTTCAT CGTGAAAATG GCACGTAAAT ACACCAACCT CCAGCAGAAA	1740
GAGGTAGGGA AGCTCAACGC CTATATGGAT GAGAGCATCT CAGGCCAAAA AGCCGTGATT	1800
GTGCTAGGAA TTCAAGAGGA TATGATGGCA GGATTTCTTG AACAAATGA GCGCGTGCGC	1860
AAGGCAACCT TTAAAGGAAG AATGTTCTCA GGAATTCCTT TCCCTGTGAT GAATGGGATG	1920
AGCCTGATTA ATACAGCCAT CGTCATCTTT GCTGGTTCGG CTGTACTTTT GAA	1973

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAAACCAAT AGTTGCTGAA GACCATAATC CAGCTGCTGT TGTTAAACCT TTAACTTTTT	60
GATTAGTTAC CATGATTGTT CCTGCCCTTA GGAAACCCAA GCCACTAATT ACTTGGGCTC	120
CCATTGCACT AGGATCACCG CTACCATAAC GACTAGTGAT GAACTGATTT GTCATCATTA	180

CAACACAAGT	TCCCAAACAA	ACTAGTAAGT	AGGTTCTAAT	CCCTGCTGCT	TGGTTTTTGA	240
CTCCTCGCTC	ATAGCCAACA	ATGCCACCGA	AAAGAATCGC	TAAAAAGCAC	CTAAGAAGTA	300
TTTCCCAAAT	ACTCAGTTCG	TATGAAAGAT	TCATATTATC	TCTTACCTCG	TTTACCTTGG	360
AATAGGCTTG	ATAAATAAAG	AGCTGCACTA	GACATAATCA	TTAAAAATTAC	AGAATAAACA	420
AACATCATTG	CCTGTGCATT	TAAAGTTGCT	GTTTCATCAG	TAGACTGTTT	AATAACGATT	480
CCCAATGGTT	GGAAAAGTGG	ATGGTACAAG	AATACAGATA	AGTCATAGTC	AGATAATAAA	540
GAATTAAAGT	TTAACACAAC	TACTGATAAT	ACGACTGGTA	AAATATACGG	TATAATAACT	600
CGCACCATAG	TGTAGAAACT	AGATGCACCC	ATACTACGTG	CAGCTTCTTC	CATATCATT	660
TCTTACTGA	AAAATACAGC	CCGAATCATT	CTATAAGAAA	ATGGTAATTT	TTGAATAGTA	720
TATGCAATAA	GTAAAAATAA	TACTGTTTCT	ACTAAACTA	AATTAAATAG	TATTAAATGA	780
GGTATATTAT	AAGTGAACAT	TAATCCTAGT	GCAATCAATG	TACCTGGCAA	TATCCATGGT	840
ATCAGTGCAC	CATACTCAAA	GAATTTATCG	AACTTACTCT	TGTTTTTATG	TACAATACGT	900
GAAATTACTA	TTGCTATAAT	TGTAGCAATT	ACCGCAGCTA	AAATTGCATA	AACAACGCTG	960
ACTAGGTAAG	GACGAAATGA	TTGAGCATCT	GTAAATAAAT	TAGCATAGTT	CGCTAACGTA	1020
AATTTAGATA	GATCTAAAGT	TCCCGTCTTG	ATCGTCAACG	AGTCTGTAAA	CGAGTATAGA	1080
ATTATCAAAA	CTATTGGTAA	CATATAGATT	GCAAACAATA	CATACGCAGC	AATGTGAGCA	1140
AGAATTATTC	CATAATGGAG	AAGAAAATTA	TCTGCTTCCT	TAATACTAGC	CTGGTTTTCG	1200
AAACAGAAT						1209

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGTCCTT	TTAGTTTTAT	CTTAATTCTC	TTATTGTTGT	AATAATCAAT	ATAGTCTATA	60
ATGGCTTGTT	CCAATTGCTT	AAGCGACTGA	AACGACTTCT	CATAACCGTA	AAACATTTCC	120
GATTTTCAGAA	TCCCAAAGAA	AGATTCCATC	ATACCGTTGT	CTTGGCTGTT	TCCCTTGCGT	180
GACATAGATG	CTTGAATTCC	CTTACTCTTA	GGAACCGATG	ATAAGAATCG	TGTTGGTATT	240
GCCAGCCTTG	GTCACTATGG	AGAATCGTAT	TCTCGTAGTG	CTTCTCTGTG	AATGCCTGTT	300
CCAACATTGT	TTGTACTTGT	TCTAAGTTGG	GTGAAGTTGA	AAGATTATAG	GCGATAATTT	360
CGCTATTAAA	GCCATCTAAA	ACTGGTGATA	AGTAAAGCTT	TTGAGTACTT	GCTGGAATGG	420
CAAATTCTGT	CACATCTGTG	TAGCACTTTT	CCATTGTTTT	AGAGCCTTCA	AATTGGCCTT	480
GAATGAGATT	CTCTGCCTTC	TTACCAACGT	CTCCTTTATG	AGAAGATTTT	GTTTCTGTGC	540
CATTTTAGCT	TGTAAATTGA	GTACTTTCAT	CAAGCCTTGA	ACTCTTTTAT	GATTTACCAG	600
ATAAGCACGA	TTCTTAGTTT	CTAAATGAAT	ACAGCGATAA	GCATAATTTT	CCTTGTGTTC	660
GATAAAAATG	GATTGAATTT	CAGCTTTAAG	CTCTTGGTCC	TTATCTGGTT	TGTNTAG	717

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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CTAAATCACC AGATTTAACC AAGTCGTAGA TACGGCCTGG TGTCCAATA ACAATATGAG      60
GCTGATTGCT TGCCAATTTT TCAATCTGGC GAGCCTTATC CGTACCACCC ACATAATTAA      120
CCACACGAAC TTCGACATCT GAGTGAGCTG AAATCTGACG CGCTACTTGG TAAATTTGAG      180
TAGCCAATCT ACGACTCGGT GCAGTAATCA CTGCTTGTA CACTATCGCTA GCTTCATCTA      240
ATTGCTGGAA AATCGGTAAC AAGAAAGTAT GAGTCTTACC TGAACCTGTT TTTGATTCTC      300
CTACTAGGTC ACGACCTGCC AAAACAATAG GAATCAACTT GTCTTGCACC TCTGTTGGAG      360
TTGTAAATTT TAACTCCTCC AAGGCTTCTC TAATATAGTT TTAAATTTGA AATTTTCGTAA      420
ATGACATAAC ATCCTCGATT CTATCTATCT TATCAATTAT ACCATATTTT ATTCCATTAC      480
AGTAGTCTCA CTTATTTAGG CTATTTCCAG TAGCTTCTCT AGTAAGAAAA GGCTGGAATT      540
TTATAGTTCC AACCTCTTTT CAGTTATTAT TTCCAGTTTA ACATAGCATT CAAGCCATAG      600
TGATCACTCA CTTGTGGACT CTTGTTACCA TCAAATACGA CATGTAAATT TTCCACCGCT      660
AACTCTTTGG TAGTAAAGAC ATAATCGATT CGAAGGGGTT CAGTGTTCCT TTTCCAGCCA      720
TCAATTTTCAG GCGGAACAGT ATAGCTACCA CTTTCTCTTT GAGCAACTTC AAATGCGTCT      780
TGTAAGCCTA ATGGACTAGC TAAATAGCT TGGTAACCTT CCCTGACCTG CTGGGTTGTT      840
AAAATCTCCA G

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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CTGTTGAGAT TGTTACGAAA TAACTGAAAA TATTTAAGGA GAAAATATAT GTTGAAACAC      60
TTAAACTTAA AAGGTCACTT ATTGACAGCC ATTTCTTATA TGATTCCAAT TGTTTGTGGT      120
GCAGGATTCT TAGTTGCCAT TGGTTTAGCA ATGGGGGGTG GTGTTCTCTG CGCTCTTGTA      180
GCAGGAAAAT TCACTATCTG GGATGCTTTA GCAACTATGG GTGGTAAAGC CCTTGGTCTC      240

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TTGCCAGTTG	TTATTGCTAC	AGGTTTGTCT	TACTCGATTG	CTGGTAAGCC	AGGGATTGCA	300
CCAGGTTTTG	TTGTTGGTCT	AATTGCCAAT	TCTGTTGGTT	CAGGGTTTAT	CGGTGGTATC	360
TTGGGAGGTT	ATATAGTTGG	TTTCTTGGTT	CAAGCGATTA	TTAAAAAGGT	CAAAGTACCA	420
AACTGGATTA	AAGGTTAAT	GCCAACCTTG	ATTATTCCTT	TTGTACCTCT	TTGGTAAGTA	480
GTTTGATTAT	GATTTATATT	ATTGGGGCGC	CTATCGCAGC	CTTTACCAAC	TGGTTGACGA	540
G						541

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGAATGAG	TGTATAAGCC	CAGCCCAAGT	TTTGCATCCG	TTCAAAGTTC	CAAGACCCTT	60
GTAAGAAGGT	TGAACGCCAC	CAAACTTTTT	TACGATCTGA	TTTAGTTAAT	TGAAGTTTTT	120
CAGTCATGAT	GTTTTTCAGTC	CTTTCCTTATC	TTAGTAGTCT	TCTAGGATAT	CGCCGATTGG	180
GTCGTTAGAA	GTTGCGGCTC	CTCCGCCACC	ATTTCCACCA	GTTTTAGAAA	GGTGAAGGTA	240
GATAAGAGCG	ATAGCAACAC	CGATAGCACC	GAATCCGATT	AGAGTAATAT	CTGACACAGC	300
AGCGAGAACG	AAACCAAGAG	CGAAGAATGG	CCATACTTCA	CGAGTTGCCA	TCATGTTGAT	360
AACCATGGCG	TAACCAACGG	CAACGACCAT	ACCACCACCG	ATAGCCATAC	CATCTTTGAG	420
CCAGTCTGGC	ATGGCACTAA	GGATACTTTG	TACAGTTTCA	GTTGGTACCA	TAAGGAGAAG	480
AGCTGCAGGA	AGCGCGATAC	GAAGTCCTTG	GAAAAGTAGC	GCAATGAAAT	GCGCACGCTC	540
CACAGCGCCG	AAGTCACCTT	TTTTAGCGGC	AGCATCTGCA	GTATGAACCA	AACCAACTGA	600
AATTGTACGA	ACAATCATTG	TCAAGAAAAG	TCCAGCTACG	GCAAGAGGGA	TAGCAACCGC	660
TTGGGCAACA	CCGATACCAG	TCTTGGTAAA	GTCACCACCA	AGAACCATGA	TAATGGCAGC	720
AGCGACAGAA	GCAAGTGCAG	CATCAGGAGC	GATAGCAGCA	CCGATATTTG	ACCAACCAAG	780
GGCAATCATT	TGAAGCGATC	CACCGAGGAT	AATCCCTGCT	TCCAAGTGGA	CCTGTTACAA	840
GCCCAATAAG	GGTACAGGCT	ACAAGTGGTT	GGTGAAATTG	GAACTGGTCG	AGGATGCCTT	900
CAAGACCTGC	AAAGGAAGGC	TACAACGACT	ACTAAAACCA	TAGAAATAAT	AGACATGTTT	960
AAAATCCTTT	CATAAATAAT	GGCTTATTTG	ACATTGGCTT	TGTTAATCAA	GTCAAAACAAA	1020
TCTTTTTTTAG	AATCATTGTTG	TACTTTACGG	ACATCAAATT	CAACACCCAA	GTCACGCATT	1080
TTTTCAAATG	TAGCAACATC	TTCTTTGTCC	ATAGACAAAA	CGGTATTGAC	CAATGTTTTA	1140
CCTGTTGAGT	GAGCCATAGA	ACCAACGTTA	AGAGTCTTGA	TTGGCACGCC	GCCTTCGATG	1200
GCACGAAGGG	CATCTTGAGG	TGTTTCAAAC	AAGATAAGGG	CATGTGTTTC	TCCAAAACGT	1260
GGGTCTTTTG	AAATATCAAT	CAGTTTTTGA	ATTGGAACCA	CGTTAGCCTT	GACATTACCT	1320
GGAG						1324

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TCATAAGGAA GCTGTCGCTC GTTCCGCTAA GGTATGGACA CCACGGTGAA CATTGGCATT    60
GTCCTGCTCA TAGTAACTGT TAATAGCTTT CAGAACTACT AGTGGTTTTT GTGTCGTCGC    120
AGCATTGTCC AGATAGACCA GAGGTCATC ATTGACAATC TGATCTAAAA TTGGAAAATC    180
CTTGCGAATC GCTTCTACAT CTAACATAGG CTTCCCCTTA GCGTTTTGAC AATTTCTCTT    240
CGATAGTTGC AATCATTTC A TCACGAACTT CCTTGACTGG AATCTCCACG ATAACAGATC    300
CAAGGAAACC ACGAACAACC AAACGCTCTG CAGTTGCCTT ATCCAATCCA CGACTCATGA    360
GGTAATACAT GTCTTCTGGA TCAACTTGTC CGATAGACGC TGCGTGTCTT GCAGTGACAT    420
CATTTTCATC AATCAAAAGA ATTGGGTTAG CATCTGAACG CGCTTGGTCT GAAAGCATGA    480
GAACACGGCT CTCTTGTTGC GCATCTGCTC CCTTAGCACC CTTGATGATG TGGCCGATAC    540
CATTGAAAGT CAAAGTTGCT TTTTCAAGGA TAACCCCATG TTGTAGGATA TTTCCGATAG    600
AGTTGCAGCC ATAGTTAGTT ACACGAGTAT CAATCCCTTG TACCTGACGA CCACTTGAAA    660
GAG                                                                    663

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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CTAGTTGGAT GGCTTCAATA AAGGATGATT TGGCTGCTCC ACTATTGGCA ATGAGCTGAA    60
AACAGATATA TTCCATTTCT TCGTCATCTT ATTTCTCCTA TCCATTCAAG TGCTTGTTC    120
AGAACTTTTG CTCCATTCAT CATTCCGTAA TCCCGCATAT CAATGGTATC TACAGGGATA    180
TTTCCTGCAA TTTCTTTCAC AGCAAGTAAC TCATAACGAA TTTGTGGCCC AATTAGAATG    240
ACATCTGCTT CATGGATATT CTTTTTAGCT TCTGTCATTG ATTTTGCTTG GATAGAAATT    300
TCAATCCCAC GTTCAGTCGC ACTTTGTTGC ATTTTTTTAA CAAGCATACT TGTGACATT    360
CCCGCATTAC ATACTAATAA AATTTGTTTC ATAATCTTAA CCTTCCATTT CTTGTTCAAC    420
AACTTTGTCA TTAACTTTGA TAAATGGAAT GTATAGAAGA ACTCCAAGTG CAAAGATGAT    480

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GAATTGAACT AGAACTGCTC TCACGTCCCC TGCTGTTGCT AACCATGCAT TTAAGAATAC	540
TGGTGTAGTC CAAGGAACTT GTATAAATGC AGGACTCATG AATCCTGTAA CTGTTGCTAA	600
GTAGCTGATT AAAATACCAA GGAAGTGAAC TGTGATAAAT GGAATAGTC	649

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTGGTATTA TTTGAAATCA GATGGTTCTT ATGCAAAAAA TGCATGGCAA GGAGCTTATT	60
ACCTTAAATC AAACGGTAAA ATGGTACAAG GTGAGTGGGT TTATGATTCT TCTTACCAAG	120
CCATGGTATT ACTTGAAATC AGATGGTTCA TATGCTCGCA ATGCATGGCA AGGAAACTAC	180
TATTTGAAAT CAGATGGTAA AATGGCTGTC AATGAATGGG TTTATGATGC CACCTATCAA	240
GCATGGTATT ATTTGACATC AGATGGTTCT TATGCTTACA GTACATGGCA AGGAAATTAC	300
TATCCTAAAA TCGGATGGTA AAATGGCTGT CAATGAATGG GTTGATGGTG GACGTTATTA	360
TGTTGGCGCT GACGGAGTTT GGAAGGAAGG TCAAGCAAGT ACAGCTTCTC CTAGTAATGA	420
TAGCAATAGT GAATATTCCT GCTGCTTTAG GAAAGGCAAA AAGTTATAAT TCGTTATTCC	480
ACATGTCAAA AAAAACG	497

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAGTCTAAA TTTTAAATAA CAAAGGTCAA AGATAGTCAA TATCAGTAAT CATAACTAAG	60
TAAACAAAAA GAGGTAAAGA ATATGAATAA CAACTTTAAT AATTTTAATA ACATGGATGA	120
TTTATTTAAC CAATTGATGG GTGGTATGCG AGGATACAGT TCTGAAAATC GCCGTTACTT	180
AATTAATGGA CGCGAAGTCA CACCTGAGGA ATTTGCTCAC TATCGTACGA CTGGTCAATT	240
ACCAGGAAAT GCAGAACTG ATGTGCAAAT GCCACAACAG GCATCAGGTA TGAAACAAGA	300
CGGTGTCCTT GCAAACTAG GTCGAACTT GACAGCAGAA GCGCGTGAGG GCAAGTTGGA	360

TCCTGTTATC GGACGAAACA AGGAAATTCA AGAAACATCT GAAATCCTCT CACGCCGCAC	420
CAAGAACAAT CCTGTTTTGG TCGGAGATGC AGGTGTTGGT AAGACAGCAG TTGTGCAAGG	480
TCTAGCGCAA GCCATTGTGA ACGGAGATGT TCCTGCTGCT ATCAAGAACA AGGAAATTAT	540
TTCTATTGAT ATCTCAGGTC TTGAGGCTGG TACTCAATAC CGTGGTAGCT TTGAAGAAAA	600
TGTCCAAAAC TTAGTCAATG AAGTGAAAGA AGCAGGGAAT ATTATCCTCT TCTTTGATGA	660
AATTCACCAA ATTCTTGGTG CTGGTAGCAC TTGTGGAGAC AGTGTTCTA AAGGGCTTGC	720
GGATATTCTC AGCCAATCGA TCTCTCTCGT GGAGAATTGA CAGTGATTGG GGCAACAAC	780
CAAGACGAAT ACCGTAACAC CATCTTGAAG AATGCTGCTC TTGCTCGTCG TTCAACGAA	840
GTGAAGGTCA ATGCTCCTTC AGCAGAGAAT ACTTTTAAAA TTCTTCAAGG CATTCGTGAC	900
CTCTATCAAC AACACCACAA TGTCATCTTG CCAGACGAAG TCTTGAAAGC AGCGGTGGAT	960
TATTCTGTTT AATACATTCC TCAACGTAGC TTGCCAGATA AGGCTATTGA CCTTGTGCGAT	1020
GTAACGGCTG CTCACTTGGC GGCTCAACAT CCAGTAACAG ATGTGCATGC TGTGAACGA	1080
GAAATCGAAA CGGAAAAAGA CAAGCAAGAA AAAGCAGTTG AAGCAGAAGA TTTTGAAGCA	1140
GCTCTAAACT ATAAACACG CATTGCAGAA TTGGAAAGGA AAATCGAAAA CCACACAGAA	1200
GATATGAAAG TGA CTGCAAG TGTCAACGAT GTGGCTGAAT CTGTGGAACG AATGACAGGT	1260
ATCCCAGTAT CGCAAATGGG AG	1282

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTGATATAA TTCTTGTTTC GAAAGATTCT CCTTAGGTAT ATCTATTCCT CCACTAGTAA	60
ACGGTAATTC CAAAACAGAG TTTACTTCGT TAAATGTAAG CCAATATTTA ACTTTATCTT	120
TATACCTTTC TAAAACTGTT CGAGCAAATT TTTCATAAAA ATGAATCATT CTTCTATCA	180
ATCCATCCAT GATATTTTCT TGCTAAATAT AATGGAGTCT CATAGTGTGA AAGAGTTACA	240
AGTGTTCTA TCCCGTGAGC ATGTAGTTCA TCAAACAATT CATCATAATA TTTCAATCCA	300
GCTTCGTTAG GTTCTTCCTC ATCTCCTTTT GGAAAAATTC TACTCCATGC AATAGAAGTA	360
CGAAAAACAT TAAAGCCCAT TTCAGAAAAC AAGGATATAT CTTCTTATA TTTATGATAA	420
AAATCAATAC CTATCAATTT TAAGTTATCT TCTGTAGGAT TTTCTGTTGC TTCTCCTAAT	480
CCACCTTTGG GTAACACATC CTGAACTGAT AAGCCCTTAC CATCTTCATT ATATGCTCCC	540
TCTACTTGAT TAGCTGCAAC AGCTCCACCC CAAAGAAAAT CATCTGGAAA AATGGTCATA	600
ACTTTCTCTC ATTATAATAT TACCAGTAAT TCCTTAGAAA TGCTCGATTG TCTGATTATT	660
AGGTAATATT AATACATCTA GAAAATCATT GGTATTCGTT ACAATTACTG GTGTAAGTGT	720
TTCTGAGCCT TTAGTCTTGA TTAAATTCAA GTCCATTTCA AAAATCAACT GATTTTGA	780
AACCTGTCTC CCTTCTTCTA CATGACTAAT AAAACCTTGA CCTTTTAG	828

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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AGCTATGGTC AGACTCAGAT TGATGGCGTT GCTTATGCCA AGTACGATAT CTTCCGTTTA      60
AAGAACGGGA AAATTGTGGA GCATTGGGAT AATAAGGAAG TCATGCCTAA GGTAGAAGAC      120
TTGACCAATC GAGGGAAGTT TTAAATTGAG GACAAAGAAT GATTGAATAC AAAAATGTAG      180
CACTGCGCTA CACAGAAAAG GATGTCTTGA GAGATGTCAA CTTACAGATT GAGGATGGGG      240
AATTTATGGT TTTAGTAGGG CCTTCTGGGT CAGGTAAGAC GACCATGCTC AAGATGATTA      300
ACCGTCTTTT GGAACCAACT GATGGAAATA TTTATATGGA TGGGAAGCGC ATCAAAGACT      360
ATGATGAGCG TGAACCTTCGT CTTTCTACTG GTTATGTTTT ACAGGCTATT GCTCTTTTTC      420
CAAATCTAAC AGTTGCGGAA AATATTGCTC TCATTCCTGA AATGAAGGGG TGGAGCAAGG      480
AAGAAATTAC GAAGAAAACA GAAGAACTTT TGGCTAAGGT TGGTTTACCA GTAGCCGAGT      540
ATGGGCATCG CTTACCTAGT GAATTATCTG GTGGAGAACA GCAACGGGTC GGTATTGTCC      600
GAGCTATGAT TGGTCAGCCC AAGATTTTCC TCATGGATGA ACCCTTTTCG GCCTTGGATG      660
CTATTTTCGAG AAAACAGTTG CAGGTTCTGA CAAAAGAATT GCATAAAGAG TTTGGGATGA      720
CAACGATTTT TGTAACCCAT GATACGGATG AAGCCTTGAA GTTGGCGGAC CGTATTGCTG      780
TCTTGCAGGA TGGAGAAATT CGCCAGGTAG CGAATCCCGA GACAATTTTA AAAGTGCCCTG      840
CAACAGACTT TGTAGCAGAC TTGTTTGGAG GTAGTGTTCA TGAATAATTT AATTGCAACT      900
TTTCAGGATC GTTTTAGTGA TTGGTTGACA GCTACAATGA CATGGGTCGG TTCCTTGAGC      960
AAGAGATAGA TTAGCCAGAC AGTCATGCCC AAAATCCCTC CAGGTAAGAG CATAGACCGT     1020
TGCACATTAA GTACGATTAA AAAAGTGATA ATGGCAAGAA AACTTGCTAC TGCTTGTAAT     1080
AAAAAGGTTG TTAGTGTCAT ATTAGTTCAT CAATACCAAG GCGACAGAAG TTCCTGCCCC     1140
TAAAGCGAGG GTAATGAGCA GGGATTCAAA CATCTTACTC ATACCAGAGT TTATGTGGTT     1200
GGTCATAATA TCACGGACCG CATTGGTCAA GGCAATACCT GGTACAAACG GCATGACCGC     1260
ACCAGCTATA ATCAAATCCT GCCCCTTTGA ATGGAAAAAC CCTGTGTTAG CCGAGCCCCA     1320
AAACTGGGGC CAATTTATCC CCCAAAGACA AAAGCTCCAT CAAAGGCTGT CACAAAGGGA     1380
ATTTCGATAA ATTTTCCACA TAGAAGGAAA AGGCAAAACC AAATAAGGTC GCCACTCCTG     1440
CCCCAAGTGC TCGTAAATAT TCCGCT

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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AAGGTTCTTC GTAAATGTAC ACCATTCCGA TGCTCAAAAT GGGTTCTGAA GCTGCTGCTA      60
AATCTGCACA AGAACACGGT CTTAAATCAG TTGAAGTTAC TGTAAGAGGT CCAGGTTCTG      120
GTCGTGAGTC AGCTATTTTCG TGCGCTTGCT GCCGCTGGTC TTGAAGTAAC AGCAATTCGT      180
GATGGGACTC CAGTGCCAAC ACAATGGTGC TTCGTCCCTCC AAAACGTCGC CGTGTATAAT      240
CATCGCATT A CACTGCTTTT CGTTTAAGAG GGAGTAAC TAATGATCGAG TTTGAAAAAC      300
CAATATAAC AAAAAATTGAT GAAAATAAAG ATTATGGCAA GTTAGTAATC GAACCACTTG      360
AACGTGGCTA CGGTACAGCT CTTGGTAACT CTCTTCGTCG TGTACTTCTA GCTTCTCTAC      420
CAGGAGCAGC TGTGACATCT ATCAACATTG ATGGTGTGTT ACATGAGTTT GACACAGTTC      480
CAGGTGTTTC TGAAGACGTG ATGCAAATCA TTCTGAACAT TAAAGGAATT GCAGTGAAAT      540
CGTACGTTGA AGACGAAAAA ATCATCGAAC TGGATGTTGA AGGTCCTGCT GAAGTAACAG      600
CTGGTGACAT TTTGACAGAT AGCGATATTG AAATTGTAAA TCCAGATCAT TATCTCTTTA      660
CAATTGGTGA AGGTTCTTCT CTAAGAGCGA CTATGACTGT TAACAGTGGT CGTGGATATG      720
TACCTGCTGA TGAAAATAAA AAGGATAATG CACCAGTTGG AACACTTGCT GTAGATTCTA      780
TTTATACACC AGTTACAAAA GTCAACTATC AAGTGAACC TGCTCGTGTA GGTAGCAATG      840
ATGGTTTCGA CAAATTAACC CTTGAAATCT TGACAAATGG AACAATTATT CCAGAAGATG      900
CTTTAGGGCT TTCAGCACGT ATTTTGACAG AACATCTTGA TTTGTTTACA AATCTTACTG      960
AGATTGCTAA GTCAACTGAA GTGATGAAAG AAGCTGATAC TGAATCTGAC GACCGTATTT      1020
TAGATCGTAC GATTGAGGAA CTGGACTTGT CTGTGCGTTC ATACAACTGT TTAAAACGTG      1080
CCGGTATCAA TACTGTGCAT GATTTGACAG AAAAATCTGA AGCAGAGATG ATGAAAGTAC      1140
GAAATCTTGG ACGCAAGAGT TTGGAAGAAG TGAAACTCAA ACTCATTGAT TTGGGTCTTG      1200
GATTAAGA TAAATAAAGG AGGAATACAT GGCTTACCGT AACTAGGAC GCACTAG      1257

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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CTATTGAAAC AAGAAAAATA GAGAATCAAA GAAAGAGAAC TTATGAATAT TCAAGAAGAA      60
ATTAAGAAAC GTCGTACCTT TGCCATTATC TCCCACCCGG ACGCGGGGAA AACCAACCATC      120
ACTGAGCAGT TACTCTAACT TTGGGGGTGA GATTCTGTAG GCTGGTACGG TAAAAGGGAA      180
GAAAACAGGG ACTTTTGCTA AATCTGACTG GATGGATATC GAGAAGCAAC GTGGGATTTT      240

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TGTTACTTCA	TCTGTTATGC	AATTTGACTA	CGACGGCAAG	CGCGTGAATA	TCTTAGACAC	300
GCCAGGGCAC	GAGGACTTCT	CAGAAGATAC	CTATCGTACC	TTGATGGCGG	TGGATGCTGC	360
GGTCATGGTC	GTGGACTCTG	CCAAGGGGAT	CGAGGCTCAA	ACAAAGAAAT	TGTTTGAGGT	420
TGTGAAACAT	CGTGGCATTG	CAGTCTTTAC	CTTTATGAAC	AAGTTGGATC	GTGACGGTCG	480
TGAGCCTTTG	GATCTCTTGC	AAGAATTGGA	AGAAATCTTG	GGCATTGCTA	GCTACCCTAT	540
GAACTGGCCT	ATCGGGATGG	GGAAAGCCTT	TGAGGGCTTG	TATGACCTCT	ATAACCAACG	600
TTTAGAGCTT	TACAAAGGGG	ATGAGCGTTT	TGCTAGCCCT	AGAAGATGGA	GACAACTTTT	660
TTGGTAGCAA	TCCTTTCTAC	GAGCAAGTCA	AGGATGACAT	TGAGCTTTTA	AATGAAGCTG	720
GGAATGAGTT	TTCAGAGGAA	GCTATTCTGG	CTGGAGAATT	GACGCCTGTC	TTTTTCGGTT	780
CAGCCCTGAC	AACTTTTGGT	GTGCAGACCT	TCCTTGAAAT	CTTCCTCAAG	TTTGCTCCAG	840
AACCACATGG	TCACAAGAAA	ACAGACGGTG	AAATTGTGGA	TCCTTATGAC	AAGGATTTCT	900
CAGGCTTTGT	CTTTAAATC	CAAGCCAACA	TGGATCCTCG	TCACCGTGAC	CGTATTGCCT	960
TTGTCCGTAT	CGTATCAGGC	GAATTTGAGC	GTGGCATGAG	TGTCAATCTC	CCTCGTACTG	1020
GTAAGGGTGC	CAAATATCT	AATGTTACCC	AGTTTATGGC	GGAGAGTCGT	GAGAAATGTGA	1080
CCAATGCCGT	AGCAGGTGAT	ATTATCGGGG	TTTACGATAC	CGGTACTTAT	CAGGTTGGGG	1140
ATACCTTGAC	GGTTGGAAAA	AACAAGTTTG	AATTTGAACC	ACTGCCAACC	TTTACTCCTG	1200
AAATTTTCAT	GAAAGTTTCT	GCTAAGAATG	TTATGAAGCA	AAAATCCTTC	CACAAGGGGA	1260
TTGAGCAATT	GGTGCAAGAA	GGAGCCGTTT	AGCTTTATAA	GAATTACCAA	ACAGGTGAGT	1320
ACATGCTGGG	AG					1332

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGACGCTG	GAACAAATCC	AAGCTGACCT	GTTCCAAGAC	CAGACTTGGT	ATGCTCTGGC	60
TTATGATGGG	GCAGAAGTGA	TTGGCTTTCT	AGCTGTTTCA	GAGACTCTTC	TTTGAAGCAG	120
AAGTCCTGCA	AATCGCTGTC	AAAGGAGCCT	ATCAGGGTAA	GGGCATTGCG	TCAGCCTTGT	180
TTGCTCAATT	GCCGACAGAC	AAGGAAATTT	TCCTCGAAGT	CAGACAGTCA	AATCAACGAG	240
CGCAAGCATT	TTACAAGAAA	GAAAAGATGG	CAGTTATCGC	TGAGCGAAAG	GCCTACTACC	300
ATGACCCAGT	CGAGGACGCC	ATTATCATGA	AGAGAGAAAT	AGATGAAGGA	TAGATATATT	360
TTAGCATTTG	AGACATCCTG	TGATGAGACC	AGTGTGCGCG	TCTTGAAAAA	CGACGATGAG	420
CTCTTGTTCA	ATGTCATTGC	TAGTCAAATT	GAGAGTCACA	AACGTTTTTG	TGGCGTAGTG	480
CCCGAAGTAG	CCAGTCGTCA	CCATGTCGAG	GTCATTACAG	CCTGTATCGA	GGAGGCATTG	540
GCAGAAGCAG	GGATTACCGA	AGAGGACGTG	ACAGCTGTTG	CGGTTACCTA	CGGACCAGGC	600
TTGGTCGGAG	CCTTGCTAGT	TGGTTTGTCA	GCCGCCAAGG	CCTTTGCTTG	GGCTCACGGA	660
CTTCCACTGA	TTCCTGTTAA	TCACATGGCT	GGGCACCTCA	TGGCAGCTCA	GAGTGTGGAG	720

CCTTTGGAGT TTCCCTTGCT AGCCCTTTTA GTCAGTGGTG GGCACACAGA GTTGGTCTAT	780
GTTTCTGAGG CTGGCGATTA CAAGATTGTT GGAGAGACAC GAGACGATGC AGTTGGGGAG	840
GCTTATGACA AGGTCGGTCG TGTCATGGGC TTGACCTATC CTGCAGGTCG TGAGATTGAC	900
GAGCTGGCTC NTCTNNGGCA GGANATTTAT GA	932

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAAACTTTC GCTCATAGGC ATACAAATTA ATCCTTTGGC ATAAGTAGCC ATAAAATTAA	60
CATTTTCTGT TGTAGCTGCT TGTGCAGAAC AAATTAAGTC TCCTTCATTT TCTCTATCCT	120
TGTCGTCTAT AACAAGAACA AGTCGTCCCT TCTGCAATGC TTCTAATGCT TCTTGTATTT	180
TTCGATATTC CATTGACTGA TTATCCTTTC TGCTAAAATC CATTTTGATA TAATAGTTCC	240
TTCGATATTT CTGATTTTGG AGAGTTATCC ATCAGTTTTT GCACATATTT ACCTAAGATA	300
TCATTTTCAA GATTTACTGT ACTCCCGACT TGTTTACTCT TAAGAATGGT TTGTTTCAAG	360
GTATGAGGGA TAACAGATAC TGAAAAGTTT ACTTTGGAGA CTTTAGCGAC AGTCAGACTA	420
ATGCCGTCOA TTGTAATAGA TCCTTTTTC AACTATTAAAT CTAAAATTC TTTTGTGTG	480
TTGATTTGAT ACCATACAGC ATTATCATCT TTTTATTATTG ACGAGATTTT TCCTGTACCA	540
TCAATGTGTC CTGTAACGAC GTGACCCCA AGTCGACCGT TGACAGATAA GGCTCTTTCT	600
AGATTCACCT CACTTCCATG TTTTAATAGA GTAAGAGCTG TTCGACTCCA TGTTCATTC	660
ATTACATCAA CTGTAAAGGA TTGATGATTG AAATGAGTAA CTGTAAGACA GATACCATTT	720
ACTGCTATAC TATCGCCTAA ATGGATATCC GTTAATATTT TTGAGGCTTT AATTGATAGT	780
TTACAATTAC GAGAGTCTTT CTGTATTCCCT TCAACTTTTC CGATTCTTTC AATTATTCCT	840
GTGAACATGG ATAAATCACT TCACTTTCTA TGAGATAGTC NTTTCCTNTT TGAGAAAAAG	900
CATAAGGTTT CAATCTAATA GCGTCATTTG GCAAAGAAAT GCCTTCACCT CCGACAGGAA	960
ACTTGGCACT GCCTCCAAA ATTTTGGTG CAATATATAT TTTCAGCTCA TCAACAATTT	1020
GTTGTTCCAA AGCACTCCAA TTCATTAGAC TGCCCCCCTC TACAACCTAGG CTATCAATCT	1080
GCATGTTTCC TTAGATGTTN GCATTAACT CNGATAAGTC TATATGATTG CCTTTTCTCT	1140
TTATGGAAAG TATTCCTC	1158

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAAAGGCTGT	TTGGATAATG	TAACATAAAG	AAATCTTGTT	TAGCAGGGAT	TGAATAGAGT	60
TCCTGAAGTG	ATGACTTCTT	TATTAGACAT	AATGTCTGGA	CCCAAGATTA	AAAGAATGGC	120
CCCGAAGAAT	ACGAGCATCA	AAGGTAGCAG	ATGCAACAAC	TGTATCGTGG	AAGATTGAGA	180
GGAACCTAGG	TAATTTAAGA	TTGTCTAAAC	TTTCTTCTTT	CTTACCAAAG	CGTCCTGCTA	240
CTTTATCTAC	AAACCAGATT	GCAAATTGCT	GTTGGTGACC	AATCGCAAAT	CCGCCACCAC	300
CAGTCAAGCG	TTGAGTTGCC	TCAACAGTCA	TATTTGAACT	AACTGCCCAG	TAAAGTCCAC	360
AGATGATACC	AATCGCTGCT	GTACCGTAAG	CATTGCGCAA	TTGTGGTACT	AAGAATAGAA	420
CCATAAGAGA	TACTGTTGCA	GCTAGCCATG	CTGATCAATT	CCCTCAACCA	GTCCATATATC	480
TCAGCCAAGA	GAATCGAGGA	GGTCTTTGCG	GAATCTCCCG	AAAACATCCA	TTCAGAATTA	540
GAACAAAAGC	AAGTTACCAG	TGGTCGGGTT	TTACAAGTCC	AAGAATTGAC	TTTTACCTAT	600
CCTGATGCGG	CCCAGCCTTC	TCTGAGAGAC	ATTTCCTTTG	ATATGACTCA	AGGACAAATC	660
CTTGGTATCA	TTGGGGGGAC	TGGTTCTGGT	AAATCAAGCT	TGGTGCAACT	CTTACTTGGA	720
CTTTATCCAG	TAGACAAGGG	GAACATTGAC	CTTTATCAAA	ATGGACGTAG	TCCTCTTAAT	780
TTGGAGCAGT	GGCGGTCTTG	GATTGCCTAT	GTACCTCAAA	AGGTCAAAC	CTTTAAGGGA	840
ACTATTCGTT	CCAACCTGAC	TTTAGGTTTA	AATCAAGAAG	TATCTGACCA	GAAACTCTGG	900
CAGGCCTTGG	AGATTGCGCA	AGCTAAGGAT	TTTGTCACTG	AAAAGGAAGG	ACTTTTGGAT	960
GCCCTAATTG	AAGCAGGGGG	GCGAAATTTC	TCAGGTGGAC	AAAAACAAAG	GTTGTCTATC	1020
GCCCGAGCAG	TCTTGCGCCA	AGCTCCGTTT	ATCATCCTAG	ATGATGCAAC	CTCGGCACTG	1080
GATACCATTA	CAGAGTCCAA	GCTCTTGAAA	GCTATTAGAG	AAAATTTTCC	AAACACGAGC	1140
TTAATTTTGA	TCTCTCAACG	AACCTCAACT	TTACAGATGG	CGGACCAGAT	TCTCCTCTTG	1200
GAAAAAGGTG	AGTTGCTAGC	TGTTGGCAAG	CACGATGACT	TGATGAAATC	CAGCCAAGTC	1260
TATCGTGAAA	TCAATGCATC	CCAACATGGA	AAGGAGGACT	AGAATGAAAC	GACAAACTGT	1320
AAACCAGACG	CTCAAACGTT	TAGCCGTAGA	TTTAGCAAAC	CATCCCTTCC	TCCTTTTCCT	1380
AGCCTTTCTA	GGAACATTG	CCCAAGTTGG	CTTATCAATT	TACCTACCTA	TTCTGATTGG	1440
GCAGGTCATT	GACCAAGTCC	TAGTGGCTGG	TTCATCACCA	GT		1482

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTGAAGGA	TCCAGAAAGT	CGCTTATATA	TTTTATTAAA	AGACGGTCAG	GTTATTGGGA	60
CTTGACGGT	TGATTTATCG	ACTAATACGA	ATTACTTCTA	CGGTTTAGCA	ATATTGGAAC	120
CTGAACGTGG	AAAAGGCTAT	GGAAGCTACT	TAGCAAAATC	CCTCGTCAAC	CAACTAATTG	180
AGCAAAATGA	CAAGGAATTT	CAGATTGCAG	TGGAAGATAG	CAATGTAGGT	GCCAAACGTT	240
TGTATGAAAA	AATTGGCTTT	GTCAAACAGA	CTCAGGTGGT	TTATCTGAAT	GAGAAAGGAG	300
CAAGGGATTG	CGAAGTGTAG	AGATATTCGG	ACTGAAATTT	ACTTGAACCT	TTAGTGATGA	360
AACTAATTGT	TCTTGATTG	CAGCTTTCCT	GATTATGATT	TATGATTAAA	ATCTATGACA	420
CCATGTCTCG	TGATTGCGA	GAATTTGTCC	CGATTGAGGA	CGGCAAGATC	AAGATGTATG	480
TTTGTGGGCC	AACGGTGTAC	AACATATATCC	ACGTGGGAAA	CGCCCGTTCG	ACGGTAGCTT	540
TTTTGGATAC	GAATTTTCGTC	GCTATTTTGA	GTACCGTGGG	TATAAGGTTG	CCTATATTTT	600
CAATTTTACA	GATGTGGATG	ATAAGATTAT	CAACCGTGCC	AGGGAAGAAG	GCATCACGCC	660
TCAGGAGGTT	GCGGATAAGT	ACATCGCTGC	CTTTCGTGAG	GATGTGACGG	CCTTGGGCGT	720
GAAACCTGCG	ACTCGCCATC	CGCGTGTAGT	GGAGTTTATG	GCAGACATCA	TCCGTTTGTG	780
GGAAGACTTG	ATCGAGAAAG	GCTTTCCTTA	TGAGACTCAA	GGGGATGTCT	ATTTCCGTGT	840
AGAAAAATCC	CACAACTATG	CTAAATTGGC	TAATAAAACC	TTGGAAGATT	TGGAG	895

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGTTTGCCC	TTCTTTCTAA	TAAAGAATTG	GCAGAACGTG	TGGCGCAGGA	GATTGGGATA	60
GAGTTGGGGA	AATCAAGTGT	TCGCCAATTT	TCAGATGGAG	AGATTCAGGT	CAACATTGAA	120
GAATCAATCC	GTGGGAAACA	CGTCTTTATC	CTACAATCAA	CTAGTTCGCC	TGTAAATGAC	180
AATCTGCTTG	AAATTTTGAT	TATGGTAGAT	GCTTTGAAGC	GTGCGAGTGC	AGAATCTGTC	240
AATGTTGTCA	TGCCTTACTA	TGGGTATGCA	CGTCAGGATA	GAAAGGCGAG	AGCGCGTGAG	300
CCAATCACTT	CAAAACTTGT	CGCAAATATG	CTTGAAGTAG	CTGGAGTGGA	TCGTTTATTG	360
ACCATCGACT	TGCATGCTGC	GCAAATTCAA	GGATTCTTTG	ATATTCCTGT	GGATCATTTG	420
ATGGGTGCTC	CTCTGATTGC	AGATTATTTT	GAGCGTCCTG	GTATGGTTGG	TTCTGACTAT	480
GTGGTTGTCA	GCCCGGACCA	TGGAGGGGTG	ACTCGTGCTC	GTAAGTTGGC	AGAATTTTGT	540
AAAACATCTA	TCGCTATTAT	TGAGAAACGT	CGTAGCGTTG	ATAAGATGAA	TACTAGTGAA	600
GTTATGAACA	CCATCGGTAA	GGTTGAAGGC	AACCACTTGT	AGCTTCGATT	GATGATATGT	660
ATTGATACCG	CTGGAACGAT	TTGTCATGCG	GCAGATGCTC	TTGCGGAAG		709

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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CTAGAAGAAC TCCGTCACAA GCTTGTGACT TGTAAGCAAG AACAGAGCAA GATTGAGGAT      60
TCCTTATGAT TTCATTCCCTT CTTCTATTGG TCTTGGTTTG GGGATTTTAT ATCGGCTATC      120
GGAGAGGCCT GCTCTTACAG GTTTATTACC TGATTTCAGC CATGGCATCG GCTTTTATGG      180
CTGGCCAGTT TTATAAGGGG CTTGGAGAGC AATTCCATTT ATTGCTCCCT TATGCAAATT      240
CGCAGGAAGG TCAGGGGACT TTCTTTTTC CATCGGATCA ACTCTTTCAG CTGGATAAGG      300
TCTTTTATGC AGGTATCGGC TACTTGCTTG TATTGGGGAT TGTCTATAGC ATTGGTCGTT      360
TGCTTGGTCT TCTCTTACAC TTGATTCCCTA GCAAAAACT GGGTGGTAAG TTGTTCCAAG      420
TTTCAGCAGG TATCTTGTCC ATGTTGGTGA CCTTATTTGT CTTGCAAATG GCCTTGACAA      480
TCTTGGCGAC CATCCCCATG GCAGTTATAC AAAATCCTCT TGAAAAGAGT ATCGTCGCAA      540
AACACATCAT CCAGAGCATA CCGATAACAA CCAGTTGGCT CAAACAAATC TGGGTGACAA      600
ATTTAATCGG ATAAAAAGGG CAGGAGTTTT CCTAGCCCTT TGTTTACAGA TTTGACTCGA      660
ATCTATCAGA ATGTAAAAAG CTACCACACC TAGACATTCA AAGACAAGGA AATAAAGATG      720
AATAAGAAAA TATTAGAAAC ATTAGAGTTC GATAAGGTCA AGGCCTTGTT TGAGCCTCAT      780
TTGTTGACCG AGCAGGGCTT GGAGCAATTG AGACAG                                816

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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CTTGAAGCAG CTGAAAGCAT GGGGTCTTCG GGATTTAAAA CCTATTCGTA ACGGGTTGTT      60
TTACCTTTCC TAGTTCCAAC CTTACTAGCA GTCCTTGCT TGTATTTATG AGAGCATTCCT      120
CAGACTTTGG AACGCCTATG TTGATTGGCG AAGGATATCG GACTTTCCCT GTCTGATTT      180
ATACCCAATT TATTAGCGAG GTTGGAGGAA ATTCTGCTTT TGCAATTATG GCGATTATCA      240
TTGCCTTGGC AATTTTCCTT ATCCAAAAAC ACATTGCAAA CCGCTACAGT TTCAGCATGA      300
ATCTGCTCCA TCCAATTGAG CCTAAAAAAA CTACAAAAGG AAAAATGGCT GCCATTTATG      360
CAACAGTCTA CGGAATTATC TTTATCTCTG TTTTACCTCA AATCTACTTA ATTTATACCT      420
CTTTCCTAAA AACATCAGGT ATGGTATTTG TTAAAGGTTA TTCTCCAAAC AGTTACAAGG      480

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TAGCTTTCAA	TCGTATGGGA	TCTGCTATTT	TCAATACCAT	TCGTATCCCT	TTGATTGCCT	540
TAGTTCTAGT	TGTTCCCTATT	TACGACATTT	ATCTCCTACC	TAGCCGTTAG	AAAACGGAAT	600
TTGTTTACAA	ACTTAATTGA	CAGCCTCAGT	ATGGTACCCT	ATATTGTACC	AGGAACCGTT	660
CTAGGGATTG	CCTTCATTTT	TTCCCTCAAT	ACTGGTCTAT	TTGGAAGTGG	ATTTCTTATG	720
ATTACAGGGA	CTGCTTTCAT	CTTGATTATG	TCTCTATCTG	TCAGAAGATT	ACCGTATACT	780
ATTCGCTCAT	CTGTTGCTAG	CTTACAACAA	ATAGCACCAA	GTATTGAAGA	AGCTGCTGGA	840
AAGCTTAGGA	AGTAGTCGTC	TCAATACCTT	TGCTAAGATT	ACAACTCCAA	TGATGCTATC	900
TGGTATCATT	TCTGGAGCCA	TCTTATCTTG	GGTCACAATG	ATTTCAAAAC	TCTCTACTTC	960
TATCCTCCTC	TACAATGTCA	AAACAAGAAC	AATGACTGTA	G		1001

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGGTTTGCA	ATCTATTCCA	ACTGAGATT	CAGAGGCAGC	AAGGATTGAT	GGTGCGACTA	60
GCAAGCAAGT	TTTCTGGAAC	ATTGAATTGC	CTTACTTGCT	ACCAAGTGTC	TCTATGGTCT	120
TTATCCTAGC	CCTAAAAGGT	GGGCTGACTG	CCTTTGACCA	AGTCTTTGCC	ATGACCGGTG	180
GTGGTCCAAA	CAATGCCACA	ACCTCACTTG	GGCTCTGGT	TTATAACTAT	GCCTTTAAAA	240
ACAACCAATT	CGGTATGCC	AATGCCATTG	CCGTAATCTT	GTTCTCTTA	ATTGTAGTGA	300
TTTCGATCAT	CCAATTGAGA	GTATCTAAGA	AATTTGAAAT	TTAAGAGGAG	AAGCATGATG	360
AAACAAGATG	AAAGAAAAGC	CCTGATTGGC	AAATACATTC	TATTGATTCT	AGGATCGGTT	420
CTGATTTTAG	TGCCGCTCCT	TGCTACCCTC	TTTAGTTTCT	TTAAACCCAC	TAAGGATATT	480
GTAGATAATT	TCTTTGGCTT	TCCAACCAAC	TTACATGGG	ACAACTTTAG	CCGTCTCTTA	540
GCTGATGGGA	TTGGAGGCTA	TTATTGGACT	CTGTCGTCAT	CACTGTCTTG	TCTTTACTTG	600
CAGTAATGAT	CTTTATCCCT	ATGGCAGCCT	ACTCCATCGC	TCGCAATATG	AGTAAAAGAA	660
AAGCCTTTAC	CATTCATGTA	TACCCTCTTA	ATCCTCGGAA	TCTTCGTACC	TTTCCAAGTC	720
ATCATGATTC	CGATTACGGT	TATGATGAGT	AAACTCGGTT	TGGCTAATAC	CTTTGGTTTG	780
ATCTTGCTCT	ACTTGACCTA	TGCGATTCCA	CAGACCCTCT	TTCTCTATGT	TGGATATATC	840
AAAATCTCGA	TTCCAGAAAG	TCTGGATGAA	GCAGCAGAGA	TCGATGGGGC	TAATCAATTT	900
ACAACCTATT	TCCGCATCAT	NTTCCCAATG	ATGAAACCGA	TGCATGCGAC	AACCATGATC	960
ATCAATGCCC	TTTGGTTCTG	GAATGACTTC	ATGTTGCCAC	TCCTTGCTCT	GAACCGGGAT	1020
TCCAAAATGT	GGACTCTGCC	TTTGTCCAA	TACAACTACG	CAGG		1064

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTAAAAGA AGTTAATCAA GTTGATAAAG CACTTTTAAA ACAAATTGGT GCAGTTGATG	60
TCTTAGAAGT GAAGGGTGGC ATTCAAGCAA TCTATGGAGC AAAAGCAATC TTATATAAAA	120
ATAGTATTAA TGAAATTTTA GGTGTAGATG ATTAAGTACT TACTGACTTA ATAAAAACA	180
GAGGAGAGTG ATGGATGAGT AGGATGAAAT GAAATCGCAT ACAAGAAATA AAGAACTCAT	240
TATCCAAGTT GGATACGCTT ATTACATAGG AGAATACAAA TGAAATTTAG AAAATTAGCT	300
TGTACAGTAC TTGCGGGTGC TGCGGTTCTT GGTCTTGCTG CTTGTGGCAA TTCTGGCGGA	360
AGTAAAGATG CTGCCAAATC AGGTGGTGAC GGTGCCAAAA CAGAAATCAC TTGGTGGGCA	420
TTCCAGTAT TTACCCAAGA AAAAAGTGGT GACGGTGTTG GAACCTATGA AAAATCAATC	480
ATCCAAGCGT TTTGAAAAAG CAACCCAGAT ATAAAAGTGA AATTGGAAAC CATCCACTTC	540
CAGTCCAGTC CTGAAAAATC ACAACAGCCA TCCGAAGCAG GAACAG	586

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTAGTTCT TCCTAGTGCA GGGGCTGTAG ACCCAGTTGC GACCCTAGCG CTGGACTAGT	60
CGAGAGGGTG TTGTTGAAAA TGGATGGNTA TCGCTATGTT GGTTATCTAT CAGGTGACAT	120
CCTCAAAACG CTTGGCTTGG ACACTGTTTT AGAAGAAACC TCAGCAAAAC CTGGAGAGGT	180
GACTGTAGTC GAAGTTGAGA CTCCTCAATC AACAAACAAAT CAGGAGCAAG CTAGGACAGA	240
AAACCAAGTA GTAGAGACAG AGGAAGCTCC AAAAGAAGAA GCACCTAAAA CAGAAGAAAG	300
TCCAAAGGAA GAACCAAAAT CGGAGGTAAA ACCTACTGAC GACACCCTTC CTAAAGTAGA	360
AGAGGGGAAA GAAGATTCAG CAGAACCATC TCCAGTTGAA GAAGTAGGTG GAGAAGTTGA	420
GTCAAAACCA GAGGAAAAAG TAGCAGTTAA GCCAGAAAGT CAACCATCAG ACAAACCAGC	480
TGAGGAATCA AAAGTTGAAC CACCAGTAGA ACAAGCAAAA GTCCCAGAAC AACCCGTGCA	540
ACCTACACAA GCTGAGCAAC CAAGTACACC AAAAGAATCA TCACAACAAG AAAATCCTAA	600
AGAAGATAGG GGAGCGGAAG AGACACCGAA ACAAGAAGAT GAACAGCCAG CAGAAGCCCC	660
AAGAAATCAA GGTGAAGAA CCAGTAGAAT CAAAAGAGGA GACTGTTAAT CAACCTGTTG	720

AACAACCAAA	AGTGGAAACG	CCTGCTGTAG	AAAAACAAAC	GGAACCAACA	GAGGAACCAA	780
AAGTTGAAGT	AACAAGTATT	CCCCAACTA	CTCGCTATGA	GGAAGACCTT	ACTAAGGAAC	840
ACGGAACGCG	TGAAGTTGTT	AAGGAAGGTA	AGAATGGCAG	TAGAACAGTT	ACTACTCCAT	900
ATATCTTGAA	TGCGACAGAT	GGTACGACTA	CAGAAGGCAC	TTCGACAAC	GATGAAGCTG	960
AGATGGAGAA	AGAGGTTGTT	CGTGTGCGCA	CGAAACCCAA	AGAAAAATTA	GCTCCAGTCT	1020
TAAGTTTGAC	AAGTGTTACA	GATAATGCAA	TGTTGCGTAG	TGCGAGACTT	ACTTATCATT	1080
TGGAATAAC	AGATAGTGTT	GATGTGAAAA	AAATTCATGC	TGAAATTAAA	AATGGCGATA	1140
AGGTTGTCAA	AACTATTGAC	TTATCTAAAG	AGAGATTATC	AGATGCTGTT	GACGGTCTTG	1200
AACTTTATAA	AGATTATAAG	ATTGTGACGA	GTATGACCTA	TGATAGAGGT	AATGGTGAAG	1260
AAACCTCTAC	GTGGAAGAA	ACTCCACTAC	GATTAGACCT	CAAGAAGGTT	GAATTGAAAA	1320
ACATCGGCTC	TACTAATCTC	GTCAAAGTAA	ATGAGGATGG	TACTGAGGTG	GCAAGTGACT	1380
TCTTAACAAG	TAAACCTGTG	GATGTGCAGA	ATTACTACCT	CAAAGTAACT	TCCCGTGATA	1440
ATAAAGTTGT	TTCCCCTCCC	AGTTGAAAAA	ATTGAAGAGG	TGACTGAGGA	AGGTCCACCA	1500
CTTTACAAAG	TCCCTGCTAA	GGCCCTAATT	TGAT			1534

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGATTTGTT	TATCTCAAGA	AGAGTCGCGA	TATTCTCCGT	GAAAGTTCAG	AATTGATTAN	60
CCAAACGGTA	GAAGATTATC	TTCAAGGAGA	TGACTTTGAC	TGGGCAGATC	TTAAAGGGAA	120
GGTTCGANAT	AATTTGACCA	AGTATCTCTT	TGACCAAACC	AAGCGTCGTC	CANCTATTTT	180
ACCAAGTAGTC	ATGGAAGCAA	AATAATCGTT	GAAATAAACA	GAGAGAAAGT	CGAGTTTCGG	240
CTTTTCTTA	TAGAAAAATA	GAAGGAGAAA	ATCATGGCAG	TAATGAAAAT	CGAGTATTAC	300
TCACAAGTAT	TGGATATGGA	GTGGGGGGTG	AATGTCCTCT	ACCCTGATGC	CAATCGAGTG	360
GAAGAACCAG	AGTGTGAAGA	TATTCCTGTC	TTGTACCTTT	TGCACGGGAT	GTCTGGAAAT	420
CATAATAGTT	GGCTTAAGCG	GACCAATGTA	GAACGCTTGC	TTCGAGGAAC	TAATCTCATC	480
GTTGTTATGC	CCAATACCAG	CAATGGTTGG	TACACCGACA	CCCAGTATGG	TTTTGACTAC	540
TACACGGCTC	TAGCAGAGGA	ATTGCCACAG	GTTCTTGAAA	CGCTTCTTCC	CTAATATGAC	600
TAGCAAGCGT	GAAAAGACCT	TTATCGCTGG	TCTTTCTATG	GGAGGCTACG	GCTGCTTCAA	660
ACTGGCTCTT	ACGACAAATC	GTTTTTCTCA	TGCAG			695

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCATCCAAG	AATAGCATAA	AAGAACTCTT	CTGTTTTTTC	TTGAGGAACG	AGAAAGTCAG	60
CAATCTCCAT	TCCACGATCC	ATCAAATCCT	CTAAAGACAT	CGTGATTTTT	AAAGTAGTAT	120
CACTAATTTG	TTTCATTTTC	ATTGCTAGTA	ACCTCATACT	TTCAGTTCTA	TCTATTATAC	180
TAGATTTTTA	CGATTTTATC	AAAAGAAGGC	TCCTCTATAC	GGATAGATTT	TCCCTAGGGT	240
CTTTCTATAG	GAGACTCCAA	GAGAAAATTT	CTGCAGACAG	ATAGAAAAAG	CCTTCAAAAT	300
CGGCTCTTAG	CCGATTTTGA	AGACCTTATA	CATCAGAATA	CTTATAATTT	AAAGGTTGCT	360
ACACCGAGGA	TAGAACGATT	TAAGTTTCTG	AGAATTTGAA	GACTTTGCTC	AAATTTCTTA	420
TAACGAATTC	ACTCCGTA	CTTCAACAAG	AAGGACTGTA	TCTCTTTCCA	AAAGAGATGA	480
TACATCCTGC	AAATCTACAA	ATGCATTCC	TTTAAAGCTT	CTTGACTCTG	TTTCAATTTA	540
TCTAGGATAG	CTTTATTTGA	GCTAACGATG	GTCAATTCCT	GTCCAGTATT	TTTGATGAC	600
AAAACATCTG	CTAGGTTAGC	AATTGTTGTA	ATCTCTGTTA	CAAAATCAAT	TTGATACTGA	660
GAAAAATCAC	CTACTCTATT	GATTGTTGGA	TTAAAGAGAT	AACTAACAC	ATTTCCCATC	720
ACAACCAAAA	TCACACAAAC	CACTCCAATA	ACAACATAAC	GAAGAATCAG	ATTTTTCACA	780
TTTAAGCCAA	GCGCTGTTTC	ACCATTTGCG	TTCAATTCTT	TAGAGTTGAT	GGTTTCCAGT	840
TTTTCAATTT	TCACATTTGC	ATAAGCATGT	TTAAATTTCT	CAATCAACCC	ATCAATTTTT	900
TTCTCTAACA	AGTCATTGGC	ATCTTTACTT	GATGTCAAAA	TTTTCACACC	AACCCCTGCA	960
TCGTCAATCA	TATAGTAGAC	GGTCAATTTT	TCCACCAAT	AGTCATTTCG	TGAATTTTTT	1020
AAGGTTGTTT	CCGTCGTGTC	TAATTCACTG	GCAATTTTTT	TCAACTCACT	GGGTTCTACA	1080
TCATTGAAAA	GATAAG					1096

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCCCATCCC	AGTGGGCAGC	AGCATTAGTC	TGTACTTCTG	CGTCGTTGCG	TTTTATTAGA	60
AGACTGATTT	TGCTTTGAAC	TACTTGAAGC	TGTCGTTGTA	TCCTGCGAAG	TTTTTGCTAA	120
CTTCAGTTTC	ATTTGCAGCG	ACATGACTAG	TTGCCAAGCC	TAGTAAACAG	ATACTTGCTA	180
ATCCAATTTT	TGTTTTCAAT	CTTTCCTCTC	CTATAAAAAA	TGTAACAGAC	ATCTGAATGC	240

TGTTCCACCT AGCTTTTGCT ACTTACTGAT TATTTTACAA AGTCAAGCAA AGCCAAGAAG	300
CTTTTCAGCTT CAAGTGACGC ACCACCTACA AGGGCACCGT CAACGTCTGG GCAAGCCATG	360
TATGAAGCAA CATTTTCAGG TTTAACAGAA CCACCGTATT GAACACGAAC TTTGTCTGCG	420
ACTTCTTGAC CAAAGTCAGC AGCTACAACG TCACGAACAA CTTTACACAT TTTTGTGCA	480
TCGTCTTG TG AAGCTGATTT ACCAGTACCG ATAGCCCAGA TTGGCTCATA AGCGATAACT	540
GAGGCAGCAA CTTGTTCAGC AGTCAATCCA GCCAATGCAG CAGATACTTG AGCACCTACG	600
AATTCAGCAG CTTTACCAGC TTCGTAAGTT TCAAGTGATT CACCACAACA GATGATTGGA	660
AGCATACCGT TCGCAAAGAT TGCTTTTGCT TTTTGTGTA TATCTTCGTC AGTTTCATGG	720
AAGTAGTCAC GCGGTTTCTG AGTGACCGAT AACACGTCAG TCAGTACCGA TTTCTTTCAA	780
AACTTGTGGG CTAGTTTCAC CAGTGAAAGC ACCTGCATTT TCTCCGTAGC AGTTTGTAGC	840
AGCGACTTTT AAGTTTGAGC CTTNGGCAAC AGCAAGNACA GTTGTCAAAT CAAGAGCTGG	900
AGCAGNGATA CCTGCTTCAA CAAGATCTGA TGAAGGAAGT TTTGATGCAA CTGCTTCAAC	960
GAATGNTCCA GCTTNTTGGG GATTTTGTGTT CATTTTCCAG TTACCAGCGA TAAATGGTTT	1020
ACGTGACATT TCACATA	1037

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTATCGTAC TAAGGATGGC AGTGTTC AAC TGTTCCGTCC TGATGAAAAT GCTAAACGCC	60
TGCAACGTAC ATGTGACCGT CTCTTGATGC CAACAAGTTC CGAACAGACA TGTTTGTAGA	120
AGCTTGTA AA GCAGTTGTCC GTGCGAATGA AGAATACGTA CCACCATACG GAATAGGTGG	180
AACTTTATAT CTTGCCCCCTC TTTTGATTGG TGTCGGAGAT ATTATCGGGG TAAACCGGC	240
AGAAGAGTAC ATTTTCACCA TCTTTGCTAT GCCAGTTGGA AATTACTTTA AAGGTGGTTT	300
GGTCCCAACC AACTTCTTGA TTCAGGATGA GTACGACCGT GCAGCACCAA ATGGTACAGG	360
TGCGGCTAAG GTTGGTGGA ACTATGCTGC AAGTCTCTTA CCAGGAAAAA TGGCCAAGTC	420
ACGCCATTTT TCAGATGTTA TCTATCTGGA CCCATCAACT CATAAAAGA TTGAAGAAGT	480
CGGATCAGCT AATTTCTTTG GAATTACAGC TGATAATGAA TTTGTAACAC CATTGAGTCC	540
ATCTATCTTG CCATCTATTA CCAAGTATTC CTTGCTTTAT TTGGCAGAAC ATCGCTTGGG	600
ATTAACCTCT ATTGAGGGTG ATGTTCCAAT TGATAATCTT GACCGTTTTG TAAAGGCAGG	660
TGCCTGTGGT ACAGCAGCGG TTATTTCTCC AATTGGAGGT ATTCAACATG GTGATGATTT	720
CCATGTTATT CTATAGTGAA ACAGAAGTAG GTCCTGTGAC ACGTAAATTA TATAATGAAT	780
TGACGGGTAT TCAGTTTGGC GATATTGAAG CGCCAGAAGG TTGGATTGTA AAAGTAGATT	840
AAAATAAACC AAAGGAGATT TTTTATGAAA TAGAAAAAGT GGCTCTTAAC AGCAGGAGTG	900
GTCCTGAGCA CGTCAGCTAT TTAGTGGCT TGTGGAAAAA CTGATAAAGA AGCAGATGCA	960
CCGACAACAT TTTCTTATGT CTATGCAGTA GATCCAGCAT CATTGGGCTA CAGTATAGCG	1020

ACTCGAACAT	CGAGGACAGA	CGTTATTGGA	AATGTTATTG	ATGGTTTGAT	GGAAAATGAT	1080
AAATACGGCA	ATGTTGCTCC	TTCTCAAAAA	GACTATGATT	TGAACAGTAC	AGGATGGGCT	1140
CCAAGCTATC	AAGATCCAGC	GTCTTACTTG	AATATTATGG	ATCCAAAATC	TGGTTCTGCC	1200
ATGAAACACC	TTGGCATTAC	GAAAGGAAAA	GATAAGGATG	TTTGTAAC TA	AACCTGGTTT	1260
GGATAAATAT	AAGAAATTGT	TAGAAGATGC	TGTTTCTGAG	ACCACTGACC	TAGAGAAGAG	1320
ATATGAAAAA	TATGCCAAAG					1340

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCTGACGGC	GTGCGCACTT	AAGAAGAGTA	TCAAAAAGAA	AAATAGAAAA	TTAACTAACA	60
AGGNAGAAAA	ACACATGTCT	AAAATTATCG	GTATTGACTT	AGGTACAACA	AACTCAGCAG	120
TTGCAGTTCT	TGAAGGAACT	GAAAGCAAAA	TCATCGCAAA	CCCAGAAGGA	AACCGCACAA	180
CTCCATCTGT	AGTCTCATT	AAAAACGGAG	AAATTATCGT	TGGTGATGCT	GCAAAACGTC	240
AAGCAGTCAC	AAACCCAGAT	ACAGTTATCT	CTATCAAATC	TAAGATGGGA	ACTTCTGAAA	300
AAGTTTCTGC	AAATGGAAAA	GAATACACTC	CACAAGAAAT	CTCAGCTATG	ATCCTTCAAT	360
ACTTGAAAGG	CTACGCTGAA	GACTACCTTG	GTGAGAAAGT	AACCAAAGCT	GTATCACAG	420
TTCCGGCTTA	CTTCAACGAC	GCTCAACGTC	AAGCAACAAA	AGACGCTGGT	AAAATTGCTG	480
GTCTTGAAGT	ANGACGTATT	GTTAACGAAC	CAACTGCAGC	AGCTCTTGCT	TATGGTTTGG	540
ACAAGACTGA	CAAAGAAGAA	AAAATCTTGG	TATTTGACCT	TGGTGGTGGT	ACATTGACG	600
TCTCTATCCT	TGAATTGGGT	GACGGTGTCT	TCGACGTATT	GTCAACTGCA	GGGGACAACA	660
AACTTGGTGG	TGACGACTTT	GACCAAAAAA	TCATTGACCA	CTTGGTAGCA	GAATTCAAGA	720
AAGAAAACGG	TATTCGACTT	GTCTACTGAC	AAGATGGCAA	TGCAACCTTT	GAAAGATGCG	780
GCTGAAAAAG	CCAAGAAAGA	CCTTTCTGGT	GTAACCTCAA	CACAAATCAG		830

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

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GTGGTGGTTT GACTGCCCTT ATCGAAGCAG GTTTCGAANT CTAAGACANA AGCAGGTTAC      60
GCTCCAGAAT TGGCTTAACT TTGAAGTTCT TCACGGAAAT GAAATTGATC GTTGACTTGA      120
TCTACGAAGG TGGATTCAAG AAAATGCGTC AATCTATTTC AAACACTGCT GAATACGGTG      180
ACTATGTATC AGGTCCACGT GTAATCACTG AACAAGTTAA AGAAAATATG AAGGCTGTCT      240
TGGCAGACAT CCAAAATGGT AAATTTGCAA ATGACTTTGT AAATGACTAT AAAGCTGGAC      300
GTCCAAAATT GACTGCTTAC CGTGAACAAG CAGCTAACCT TGAAATTGAA AAAGTTGGTG      360
CAGAAATTGCG TAAAGCAATG CCATTCGTTG GTAAAAACGA CGATGATGCA TTCAAAATCT      420
ATAACTAATT AGAAATATAT AGCGCTGGAG ATGATTTTAT GAAAAAGATT ATGAGAAAAA      480
TTGCATCGTT ATTATTGGTT CTAGTTGTAT AATGTAATTA CACCGTCGGT AATAGTGCTA      540
GCAGACCAAA ATAAAGCAGA TTGGTCGTAT GATGAAAATA CTGTAATTAA CATTATGAT      600
GATGCTAATT TTGAAGATGG TAGGTTGCAT ATGACCTTTG AACAATTCTT CAAATTGGCA      660
CAAATAG                                         667

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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CGGTTCCAGA NACTGGTATG GCTAGGAGTC GCGACAAAGT GTATCTTATG ATGGTCGATT      60
TGATACTCAA TACGCTCAAT ACTTACGGAA AGAATAAAGC ATCATTGTCA ACCGGAATAG      120
TATGATAATC GTTCTTGGT GGAATAAGTT CAATCTTATC CTTCTTAGGC ACAATAATGG      180
AAGAGCCCAG TGTTGATAA ACACGATTAT TAAGGCTGGC AATTTCCGTT AATTGCAAAG      240
CTTCAATGGT AGGGTGTAAC ACAGCACCAC CAAGAGACTA GTTATAGGCA GTACTACCAG      300
TCGGTGTCGA AACTGTTAGC CCGTCTCCAC GAAAACGTTT AAAGGGAACA CCATTTATTA      360
CAATATCTGC CACCATGGTT CGATCAGACC TGCGGATGCT GGCTTCGTTG AGTGCTCTGA      420
AAATCTTAAC TTCACCATTT TCAAGAAAGA CCTTCACATT CAGAACAGGG TAAGAAACCC      480
TTGCCCCAGT ATCTAGCTGC AAATTAGTCA CTAGCTTGTC CAACTCAAAA TCACGATAAT      540
CTGTATAGAA GCCCAAATGT CCAGTATGAA GACCGATAAA GCGGACCTTG TCAAGCTGAT      600
TTTCGTAATT ATGAAAGGCC GACAAGAGCA TACCATCCCC GCCAATGGAA ATGACAATAT      660
CCGGATTGGT ATCATTGAGT TATAAACTGA TTTCTCTTCA AACGATCTCG CAATTCATAC      720
AAAACCCTTT GACTCTGCGG TTTTCTATTG GCTATCAGAT CAATTCGTTT ACCTGTATTC      780
TTCATCTGTA TCGTCACTGN NTCCAACACC GTCATTTAAT TTTCTACTCA AAGGATCAAA      840
AAGTGCCCTGG GCTTCTTGGA TATCATCAGC AATTTACCCC ATTTCTTCAT CCAACTGATG      900
GGCGATTCTA GCTGTAATTT CCAGTCGCTT CTTAATCTCA TCTGGGAAAT CCCCTTGGTA      960
CTTGTAAGTT AGAGAATGTT CTATCGTTGC CCAGAAATTC ATGGCCAAAG TACGAATTTG      1020

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AATTTCTGCC	AAAATAGTCT	TAGCTCCATT	GATGGTATCA	ACCGTATATT	CTACTACCAC	1080
ATGATAGGAA	CGATAGCCTG	ATGCTTTTCT	ATGAGTAATG	TAATCTCGCT	CCTGTATGAT	1140
TCGCATATCC	TGACGCTTGT	GCAAAATATC	CACTACTTCC	TTGACGTCAT	CTACAAACTG	1200
AACCATCACA	CGTAAGCCAG	CAATATCCTG	CAAATCGTGT	TCCAAGGTCG	CATAAGTAAT	1260
GCCACGACGA	GCCATTTTTF	CTTTGATGCT	CTCAATTGGC	TTGACTCGAC	CGGTCACAAA	1320
CTCAATTGGA	GAATGCTTAT	TTTGCTTACG	ATATTGCTTA	CGAATACCAC	GAAGTTTAAT	1380
CTTTAACTCA	CCAACAG					1397

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCCCATGAC	ACCTGCACGC	TCCGTACGGG	CCACGTGCTT	TTTAATCCGT	TCAACAACCTT	60
CATAACCCGC	TTCAACATCC	ACACCCGACT	GGGCATATGC	ATTTTATTTT	GTCATTTGTT	120
TTTTCTTTT	CTTTAATGGA	GAATCTGTCT	CCTACTTGTA	AAAACCTGGT	TTTTCTTCCA	180
AACTTCTACG	ATAGTCTTCT	TCGTAGTCAT	AGAGAGGCGT	TGGGTAGTCA	CCGTCAAAGT	240
AAGCGACACA	GAGACCACCG	TTCGGCGCAT	CTGTTTCGAT	ACCAATCGAC	TCAATCAAGC	300
TATCAATTGA	AAGATAAGTC	AGACTGTCCG	CACCAATGAT	TTGGCGAGTT	TCTTCGACCG	360
TATGATTGGC	TGCAATCAGC	TCCTGACGGG	TCTGGATATC	AATCCCGTAG	AAACATGGAT	420
ACGCTAGTGC	AGGACTTCCA	ATGGCAACGT	GAACCTCAGT	CGCACCCGCT	TCTTTCAAGA	480
GCTGAACGAT	ACGACGAGAG	GTGTTCCAC	GTACAATGGA	ATCATCCACC	ATGACCACAC	540
GTTTGCCTTT	GACAACACCC	GAAACAGCAG	ACAGTTTCAT	CCGCACTCCT	TGCTCCCGCA	600
ATTCTTGAGT	CGGTTGGATA	AAAGTTCGCT	GGGTGTATTG	GTTTTTGATC	AGACCCATTT	660
CATTTGGTAA	GCCTGATTCT	TCCGCAAATC	CCATAGCCGC	GCTTAGGGAA	GAATTGGGCA	720
CACCAACTAC	AATATCTGCC	TCATGCTTAA	ATTCTCGCGC	CAATTGCGCT	CCCATTCTCT	780
TACGTGCCGT	ATGGACATTG	ACCCGTGGAT	ATTAGAATCA	GGGC		824

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

CTTCTTCCTT GGTACTTCCT CAATTGGATT ACCTTTGGCA TTGCTAGTTT TTCACTCCTA    60
CCTTATATCC AAGGCACTAA AATTATGTTT TACCGAGCAG TATTGGCTCG AAAACGTCCA    120
AAAGCTTGAA GGTTTTCCCC TCAAGCTTTT TTCTATCAAT GAATTTCTCC GCCTACCAAC    180
GTGAGTTCCT GATCTCCATG TTCTATCATA GCGCCGATTG CTGCTTCTAT CCCTCGCCGA    240
ATATCCACTA AACTCATAGT TGGAGTAGTC GGTCTGTTCA CCACCTGTTC CATCATATAA    300
GGAATATGCA TAAAACCTGC CTTAACATAT GGAATTTCT TTTCTACCAA ATAGAGAGCC    360
TGATACATCA AATGACTGCA AACAAAAGTC CCTGCACGTA TTGGAAACAG ACTGCCGGTA    420
AGTCCTTCTT TTTTATTAGC TTGTACCATC GCTTTGATAG GTAAACTACT AAAATAGGCC    480
GATGCTCCAT CAATACGAAT CGGTGTATCA ATTGGTTGAT TGCCTTCGTT ATCAGGTATG    540
CGAGCATCAT CTTGATTAAT AGCCACTCGT TCAGGTGTTA AGCCGGTCCCT GCCGCCTGCT    600
TGTCCAATAC AAAGTACAGC ATCTGGTTGA TATCGTAATA TTTCTGCCTC TAAAACCTCT    660
GACGACTTAT AAAAAACCGT TGGAATTTCT ACCCAGCGAA CTTCAGCCCC ATTAATCTCA    720
GATGGTAATA ATTTTACAGC CTCCAAAGCT GGATTAATCT TTTACCTCC AAAAGGATTA    780
AAACCTGTAA CCAATATTTT CATTTTATTT TCCTTTACTA AAATGCGAGA AAGTACATTA    840
AGAATATGTG AATAACAATC ATTACTAGAG CAACACCTGC TTGAGCCTTT ATAACGCCAT    900
TCTGATCTTT CATATCCATC AATGCTGCTG GTAGAGCGTT AAAATTAGCA GCCATTGGGG    960
TCAATAAGGT CCCACAATAA CCTGCTGTCA TGGCAAGAGC ACCAGCCACA ATTGGATTAG    1020

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

CTCGTAAAAA CACTAAAGGA GGTAATAAC CAATGTTAGT ACCTAAACGT GTTAAACACC    60
GTCGTGAATT CCGTGGAAAA ATGCGCGGTG AAGCAAAAGG TGGAAAAGAA GTAGCATTCG    120
GTGAATACGG TCTTCAAGCT ACAACTAGCC ACTGGATCAC TAACCGCCAA ATCGAAGCTG    180
CTCGTATCGC CATGACTCGT TACATGAAAC GTGGTGGTAA AGTTTGGATT AAAATCTTCC    240
CACACAAATC ATACACTGCT AAAGCTATCG GTGTGCGTAT GGGATCTGGT AAAGGGGCAC    300
CTGAAGGTTG GGTAGCACCA GTTAAACGTG GTAAAGTGAT GTTCGAAATC GCTGGTGTAT    360
CTGAAGAGAT TGCACGTGAA GCGCTTCGAC TTGCTAGCCA CAAATTGCCA GTTTAAATGT    420
AAATTTCGTAA AACGTGAAGC AGAATAAGGA GAAGGCATGA AACTTAATGA AGTAAAAGAA    480
TTTGTTAAAG AACTTCGTGG TCTTTCTCAA GAAGAACTCG CGAAGCGCGA AAACGAATTG    540
AAAAAAGAAT TGTTTGAAC TCGTTTCCAA CCTGCTACTG GTCCAATTGG AAACAAACAG    600

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

CTTCAGCGAC ATATCTATCC ACAACTTCTC TCGATTTCATG TTCCTCTGAA AATGCCTGAA      60
ATTTTAATTG ACTAATTTGA TCCTGATACG AACTATCTGC TAACAAAAC TCAAGATGGG      120
AAACATTTGC TAACGATAA GGTCTTCTAT CCTTACCTAA CCAAGTTTCT GTCTCTTCAT      180
CCTCTATTAG TCCCCAGTTA CTGGCAAAGT CAGGATGATT CTCTAAAAA ATACGTTCTG      240
TCTGAAAAGT GACTGACCGA ATGGGGAAAG AAGCTGTTCC TCTCTCAAAA CTAGTAAACA      300
ATGCACGCGC AATCCCCTGA CGGCGATGAC CTGGATGAAC CAGTATCGTC ACTTCTACAT      360
CTTGGTCATC TGCATAGACA GTTAATAAAC CAACAAGTTC GCCTTTTTTCA TAATAAAGGA      420
AAAAGGCGGG CATGTTTGGG TCAAAATTAA GCATGTTAGA GAGATAGGGA TCGCGATAGG      480
TACCGTCATA GTTTTGCGAA CAGTTAATTA CTTTTTTCGC CTCAGATAGC TCTTCTTGGC      540
TTAACTTGTT TCTTGCTTGA ATCATATAGG TATCCTCTAC AAACCAGACG ATCTGTGACT      600
GGCATCTTTA GCCTGCTCGA GTTTATTGAC ATAATACTCC CGTTTTTCTT CGACTTCGTG      660
AATAACAGGC TCATCTTTCT TACCATGAAG ACGGACAATC TTGGCCGGAA TACCGACAAC      720
CGTCACATCA CTAGGTACAT CTGCTACGAC AACTGCTGCA GCACCGACCT TGGCATTTTC      780
ACCAATTTCC ACAGGCCCGA TAACTTGGGC ATGGGCTGAT ATGAGGGCTC CCTTTCGTAC      840
AGTCGGATGG CGTTTGCCAC AGTCTTTCCC TGTTCCTCCG AGAGTCACTC CGTGATAGAG      900
AAGAACGCCT TTTTCAACAA TCGCTGTCTC TCCAATCACC AGACCAGAAC CATGGTCAAT      960
AAAGACACCT GAATCAATCT GGGCTCCTGG ATGAATCTCA ATCTGAGTCC AAAAGCGCCA     1020
AAACTGACTG TGCATACGAG CTAAGAGTTT GAAGTCGTAC TTCCAGAGAA AATGCGAGAG     1080
ACGGTGGGCC GCCAAGGCCT TGACACCTGG ATAAGTCAGC AAAACCTCCA AAGTGGTGCG     1140
GGCCGCTGGA TCATTTTCTT TTACGATATC AATGGTTTCG CGCCACCACC CCATACATTT     1200
CTCCTTTTCT TACTCTGAAT CTT                                     1223

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(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

GGTGAGTGCC TTTATTAGCG GAGCTTCTCA AGTGATTGTT GCCTTGATTA TCTTCCTTTC      60
ATGCTCTTTT ATCTCTTGCG TGATGGGAAA GGCTTGCGTA ACTATTTGAC CCAATTCATT      120
CCAAGCAAAT TGAAGGAACC TGTTGGACAA GTTCTATCAG ATGTGAATCA ACAGTTGTCC      180
AACTATGTTC GAGGGCAAGT GACAGTGGCT ATTATTGTAG CAGTAATGTT TATCATCTTC      240
TTCAAGATTA TTGGTCTACG CTATGCGGTT ACGCTGGGGG TTACTGCTGG TATTTTAAAT      300
CTGGTCCCTT ATCTTGGTAG CTTTCTAGCC ATGCTTCCTG CCCTAGTATT GGGTTTGATT      360
GCTGGTCCAG TCATGCTTTT GAAAGTAGTG ATTGTCTTTA TTGTAGAACA AACTATTGAA      420
GGCCGTTTTG TCTCTCCATT GATTTTGGGA AGTCAATTAA ACATCCACCC TATTAATGTT      480
CTCTTTGTTT TGTTAACTTC AGGATCTATG TTTGGTATCT GGGGAGTTT ACTTGGTATT      540
CCGGTTTATG CCTCTGCTAA GGTGTGCATT TCAGCCATTT TCGAATGGTA TAAGGTAGTC      600
AGTGGTCTAT ATGAATTAGA GGGTGAGGAA GTCAAGAGTG AACAATAGTC AACAGATGTT      660
ACAGGCTTTG GAGGAGCAAG ATTTAACTAA GGCTGAGCAT TATTTGCGCA AAGCTTTAGA      720
AAATGATTCA AGTGATCTTC TGTATGAGTT GGCAACTTAT CTTGAAGGGA TTGGTTTCTA      780
TCCTCAGGCC AAGGAAATTT ACCTGAAAAT TGTAGAAGAT TTTCCAGAGG TTCATCTTAA      840
TCTAG

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CTATGGATTA ATCTTCTTCT ATCTTATCCT GTTCCTAAAT ATGTTGGTAG AAAAATGAAG      60
CAGTTGTTAC GAGTGTCTGT ATTGGAAAAA AATTTTGTCT ATACAATTCT TTAAATGATA      120
TGAAGACTAG GAATGCCAAA AACTGACAT ATTCGTTTA AAGCCTATCC AGTCTCTTCA      180
ATTGTATTTG TAGAAATGCT ATCAGTAATA TATTCGCGAA CACTATGATT TACAACAGTG      240
TGGTCGTACA TCTTTGTAAC TTTATTATAC AACAACCATT TACAGGTGTA AAGTTGAGCA      300
GTGTCTTTAG TAAATTTAGG GACTTGTTTT GTCATAGTTT TGATACCTGT ATTCGTTGTT      360
TCATGAGTAT TTGACGTTTC TTTTCATGTA GGCATTTCAA CAATTAGAAT GATATTTTTC      420
CGAGGATGAA CTTATATATT ATGACTTTTT AGAGTTATGA TGCTCTTGA TTTGACTATC      480
GCTATCAATT TCATCCACTT TTACAGTTTC ATGCAACATA GCGAGAAGGC GGTTCCTAT      540
ATGGAAGTCG TCTTGTTTTC ATATTGTCTA AATACGAGAT ATTTACTACA GGTGTAGAT      600
ATTGCAAGCT CAAATGATAT TATTTTAGAG GAGGAGACAA GTGAAATAAT GCCTGGTGAG      660
TTAGATGAAA TAAAAAGTAA GGAGTTGAAA GTACTGGTTC NTTGTGCAGG GTCTGGAACA      720
AGTGCGCAAT TAGCCAATGC AATTAACGAG GCGGCTCNAT TAGCAGAAGT TAGAGTGATT      780
GCGAATTCAG GAGCGCACGG AG

```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CTGGGACTCT CTTCGTAGAA GTCATGCAAG AATATTTTGA TCAAAAGAGG AAATCATGAA      60
AAAAAGAGCA ATAGTGGCAG TCATTGTACT GCTTTTAATT GGGCTGGATC AGTTGGTCAA      120
ATCCTATATC GTCCAGCAGA TTCCACTGGG TGAAGTGCGC TCCTGGATTG CCAATTTTCGT      180
TAGCTTGACC TACCTGCAAA ATCGAGGTGC AGCCTTTTCT ATCTTACAAG ATCAGCAGCT      240
GTTATTGCGT GTCATTACTC TGGTTGTCGT GATAGGTGCC ATTTGGTATT TACATAAACA      300
CATGGAGGAC TCATTCTGGA TGGTCTTGGG TTTGACTCTA ATAATCGCGG GTGGTCTTGG      360
AAACTTTATT GACAGGGTCA GTCAGGGCTT TGTGTGGAT ATGTTCCATC TTGACTTTAT      420
CAACTTTGCA ATTTTCAATG TGGCAGATAA CTATCTGACG GTTGGAGTGA TTATTTTATT      480
GATTGCAATG CTAAAAGAGG AAATAAATGG AAATTAAAAT TGAAACTGGT GGTCTGCGTT      540
TGGATAAGGC TTTGTCAGAT TTGTCAGAAT TATCACGTAG TCTCGGAAT GAACAAATTA      600
AATCAGGCCA GGTCTTGGTC AATGGTCAAG TCAAGAAAGC TAAATACACA GTCCAAGAGG      660
GTGATGTCGT CACTTACCAT GTGCCANAAC CAGAGGTATT AGAGTATGTG GCTGAGGATC      720
TTCCGCTAGA AATAGTCTAC CAAGATGAAG ATGTGGCTGT CCTTAACAAA CCTCAGGGAA      780
TGGTTGTGCA CCCGAGTGCT GGTACATACCA GTGGAACCCT AAGTAAATGC CCCCCATGTA      840
TCATATTAAG GACTTGTCGG GTATCAATGG GGTCTGCCT CCANGGATTG TTCACCCGTA      900
TTGATAAGGA TACGTCACGT CTTCTCAT                                     928

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(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CTCTTTTACA GAGGTGTTTC CTATTTGTG CTTCCATTTT TGGGGCAAGG AATTGTAGAT      60
GGGGATGGCA ATCCTATCTT TTTATTGATT ATGATATTCG TTTGCTTCAT AGTTTTAGTC      120

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TTTTTGAAAT GGTTAGACTA TGATTTCACT AGATTGAGAA GGGAGTTTCT AGATACAGGT	180
TTTCAAAAGT CTCTTACTAA GATTAAGTGG GCAATGGGGG CTTATTATCT AGTGATGCAA	240
AGTCTATCTT ACCTTGAATA TGAACAAGGT ATTCAATCAA CGACTGTTTCG CCATCTCATC	300
CTAGTGTTTT ACCTACTCTT TTTTATGGGG GGTATCAAGA AATTGGATAC CTATTTGAAG	360
GAAAACTTC AGGAGGAACT GAACCAAGAG CAGACCTTGC GCTACAGAGA TATGGAACGC	420
TATAGTCGGC ATATAGAGGA ACTTTACAAG GAAATTCGGA GTTTTCGCCA TGACTACACT	480
AACCTCTTAA CCACTTACGT TTGGGCATTG AAGAGAAGGA TATGGAGCAG ATAAAAGAGA	540
TGTACGACTC GGTCTTAAGG GATTCCAGTC AGAAATTGCA GGACAATAAA TATGACCTGG	600
GCAGATTGGT GAATATTNGT GACCGTGCCC TCAAGAGTCT CCTAGCTGGA AAATTTATAA	660
AAG	663

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGATTAAT CTGATATTTC TTTTGGCAA ACCAAATGCT TCCTATCAGA AAAGCTAGCA	60
ACAGCAACAT GGTAATAATG ATATGAATGG TCATTTTCTT CTCCTATTCT GCCTTTTCAA	120
TATCTTTTTT CATCTCGTCA ACATTGAAGT TAGCAAACAA GTATTGACGG TCTTGGACTG	180
GGAAACGTTG GTCCAACTGG TCAACTGCTC CCACCTCGAT AATGCCTTCC TTGATGACAA	240
AATCCATGAC ATGTCCACCG AAGGTCAAAT CATCTGATAT GAAGTGCAGA TGGTAGCCTG	300
CCCACTGAC CCCATGAAA ATCTCAGGCG TCCAGAAACC AACAAAGTC CCCGCAACAT	360
TGTCACGACT ATATTCCGGT TGATGGGTTG CGACATCAGC AAACCTGGTA TCGGGTGTTG	420
ACTTAGGAAT CATACGCACA TGCATATGTT AAAAATTCCC CCCCGAATCT TGATAGAGCG	480
GAAAAGATTT TCCCCATCAT AATAAGACTC AATTCGTTCT TTCAATTCCT TGTCTGTCAT	540
CTCAAAGCGC TGGCGAAAAA TGACCTCTGC CTGATGCGGT ACCACTGCAG CGTAAGGAAT	600
AAGGGCATCT GGTGACACTT CCACAATTTC TGGCTGGTCT CCTGACCCTT TGG	653

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTACGATATC	TTTGGTCTTT	TGTAAGATAT	GAGGTCCACC	CTTATGCGCC	TCAGTTGGCA	60
TTTCATGCGA	TTCAAGAAGT	TGCCCCCTCT	GATCAACCAA	ACCATACTTG	ATGTTGGTTC	120
CACCGATATC	AATTGCAACG	TAATATGTCA	TAAATACCTC	CTTTTAGATT	AGAGGAAGCG	180
CTCCTTGGTT	TCACGAATCA	AGGCAGCAGC	CGCTTCTACA	ACTGGACGAT	CTTCTTCAGT	240
CACTGGTGTC	AATGGTGAAC	GAACAGATCC	AATATTCAAG	CCTTCATTGA	TTTTCAAGAC	300
TTCTTTGATG	ACACCGTACA	TATTTCCATG	AGCAGAAGTG	AGTTTACCAA	TGATTGCGTT	360
GATAGCATAC	TGCAATTAC	GCGCTGTTTC	TAGGTCCTTA	TCCGCAATCA	ACTGATTGAG	420
TTTCAAGAAG	AGTTCTGGCA	TAGCACCATA	AGTACCACCG	ATACCAGCCC	TAGCCCCCAT	480
GAGGCGTCCT	CCTAGGAACT	GCTCATCAGG	ACCATTAAAG	ACGATATGGT	CTTCTCCACC	540
AAGGCTGACA	AAGGTTTGA	TATCTTGAAC	TGGCATAGAA	GAGTTCTTCA	CACCGATAAC	600
ACGAGGATTT	TTCAACATTT	CTGTGTAAAG	GCTTGGAGTC	AAAGCAACCC	CTGCCAATTG	660
AGGAATGTTG	TAAATCACGT	AGTCTGTGTT	TGGAGCTGCA	GAAGTATGAT	CGTTCCAGTA	720
TTTGGAACCT	GAGTTATTCT	GGCAAGCGGA	AATAAATTGG	TGGAATCCGT	TGCAATAGCA	780
TCTACTCCCA	AGCTTTCAGC	ATGGCGAGCA	AGTTCCATAC	TATCTTTAGT	ATTATTGCAA	840
GCAACATGGG	CAATAATGGT	CAATTTACCT	TTGGCTACCG	CCATGACTTC	TTCCAAAATC	900
AACTTGCGAT	CTTCAACGCT	TTGGTAGATA	CATTACCAG	AAGAACCATT	GACATAAGAC	960
CTTGAACACC	TTTATCAATG	AAGTATTGA				989

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCAAAGAGTA	ACAAAGGCAC	CAAATTCTCG	ATAGGAACGA	TTTAGCACGG	TAAACTTCAT	60
CCACTTGGGT	TCACGGAACC	AAACCAGCAA	TAATTTCTTT	GGGCACGGGT	TAATAGCATT	120
TTGGTCAACT	AGGAGTAGAT	AGAACACATT	TCNTTCTTCG	TCTATATCAA	TCTTAACACC	180
TGTTTCAGCG	ATAATCTTGT	CGATGGTTTC	TCCACCCTTA	CCGATGACAA	TCTTAATCTT	240
GTCCACATCA	ATCTTGATCG	TATCAATTTT	CGGAGCAGTT	GGAGCCAATT	CTGGACGAAC	300
TTCTGGAATG	GTTGCTTCAA	TGACATCAAG	GATTTCAAAA	CGCGCTTTCT	TGGCTTGAGC	360
AAGAGCCTCC	GTCAAGATTT	CTGCAGTAAT	CCCTTGAATC	TTGATATCCA	TTTGAAGGGC	420
TGTAATCCCA	TCACGAGTAC	CTGCAACCTT	GAAGTCCATA	TCTCCAAAGT	GATCTTCCAA	480
ACCTTGATA	TCTGTCAATA	CTGTGTAGTT	ATTTCCATCT	GAGATAAGTC	CCATAGCAAT	540
ACCAGCTACT	GGCGCCTTGA	TTGGCACACC	ACCAGCCATA	AGGGCAAGAG	TTCCCGCACA	600
GATAGAAGCT	TGAGATGAAG	AACCGTTTGA	TTCCAAAAC	TCTGCTACTA	GACGGATAGC	660

GTATGGGAAT TCTTCCAAGC TTGGCAAGAC TTGAGCAAGA GCACGCTCAC CAAGGGCACC	720
GTGACCGATT TCACGACGAC CTGGCGCACC GTAACGACCT GTTCCCTTA CAGAATATTG	780
AGGGAAGTTA TAGTGGTGCA TAAAGCGTTT CTTGTACTCT GGATCCAAAC CATCAATGAT	840
TTGAGTTTCT CCCATCGGAG CCAAGGTCAA GACTGAAAGA GCTTGAGTTT GCCCACGAGT	900
AAAGAGACCT GAACCATGTT ACACGAGGAA GGAAGTCAAC AACC GCATCC AAAGGACGGA	960
TTTCATCGAC CTTACGACCA TCAGGACGCA CCTTGCTCTC TGTAAATAAA CGTCGCACTT	1020
CTGCGTGTTC CATTTGTTC CAGATTTTCT CCACATCACG CATAATACGG TCAAATTTCTT	1080
CGTGGTCCGC ATATTTTCT TCGTAAACGG CAGTCACTTG GTCTTTTCACT GCTTGAGTTG	1140
CAGTTCACGG GAATCCAATT TCTCTTCTAC TTGAACTGCC TTTTGAGGT CACTGTTGTA	1200
GGCTGCAATG ATTTTCTGCT GCAATTCAGC ATCCACGTGA AGCAATTCCA CTTCTGCTTT	1260
TTCTTTTACC ACAGCAGCAA CGATTTCTTC TTGGAAGGCA ATCAATTCTT TGACAGCTTC	1320
GTGCCCCTTA AGAAGCGCTT CCAACATGAT TTCTTCTGAC AATTCTTTGG CACCAGACTC	1380
TACCATGTTG ATAGCGTGCT TGGTTCAGC TACTGTCAAT TCAAGAAGAG ATTGCTCTGC	1440
TTGTTCTTGA CTTGGGTGTA TGATGATTTG GCCATCTACA TATCCCACTT GTACCCAGC	1500
AATTGGTCCG TCAAATGGAA TATCTGAAAT AGACAGTGCC AAAGATGAAC CAAACATAGC	1560
AGCCATTGGT GCAGATGCAT TTTCATCATA AGAAAGCACT GTATTGATGA CTTGGACTTC	1620
ATTACGGAAA CCTTCCGCAA ACATAGGACG AATCGGACGG TCAATCAAAC G	1671

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCAGTATCT TTGTAATCAA CATATCCAAT TTTGTTTGCT GCGATGTANT CAACTTTTTT	60
ACGGCGTTTG AATCCGCCAC GACGTNGTTG AGCCATGTTT TTNCTCCTTT ATAAGTTTAG	120
TTGTCCATTA GAATGGTAAA TCATCANCTG AAATATCCAA TGGGTTTGTT GCTCCAAATG	180
GATTTTCATT ACGTGAAAAG TCTGGTACTG AATTTGTAGG TGCTGAATAG TTTGCAGTTG	240
GTGCAGAGTA AGCTCCACCT GTGTGACCT CACGCACACT ACGGCTTTCC AACATTTGGA	300
AATTCTCAGC CACGACCTCT GTCACGTAGA CACGTGTGCC TTGCTGGTTA TCGTAACTAC	360
GAGTCTGGAT ACGACCTGTC ACCCCGATAA GTGAGCCTTT TTTAGCCCAG TTAGCAAGAT	420
TTTCAGCCTG TTGGCGCCAC ATAACGACAT TAATAAAATC AGCCTCACGT TCACCATTTT	480
GACTCTTAAA TGTACGGTTT ACTGCAAGAG TAAAAGTCGC AACTGCTACA TTTGATGGGG	540
TATAACGCAA CTCAGCGTCA CGTGTACATC GCCCTACAAG TACAACATTG TTAATCATAG	600
TTTACCTTCT TACGCGTCAA TTTTGACGAT CATGTGACGA AGAATGTGAG CGTTGATTTT	660
GGAAAGACGG TCAAACCTCT TAGAGAGCTG CATCGNTCAT TTGCTTCAAC GTTAACGATG	720
TGGTAAAGTC C	731

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

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CTGGGTTTTA CCACGTTTTC CTGATGTACG AGCGAGATCC TTACGGTTCA ACATAGTGTT      60
GATAAAGCTG GATTTACCAA CATTTGAACG CCCTGCTAGG GCAATCTCTG GCAGTTCATC      120
CTGCGGATAG TGGGACTTAT TAGCTGCACT GAGCAAGATT TCAGCATTTGT GTGTATTAAG      180
TTCCATAGTC ACCTCTAGGC TGTTTCTAGG ATCGGTTTAT CCGTTCCATC GACAGTTTCT      240
TTAGTGATGC GAACCAATTT CACATTTTCC TGACTCGGCA CCTCAAACAT AACATCTAGC      300
ATGGTTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCCTG TCTTCCGTTT GATTGCTTTA      360
TTAGCAATCT CTTGAAGGGC TTCGTCGTCA AATTCCAACCT CAACATCATC ATAAGAAAGC      420
AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT TCAAGATGCG AACCAAGTCC      480
ATCAACGGAC AATTGCTCAA GAGCCGCAAA AACAGGCAAG CGTCCAATCA ACTCAGGGAT      540
AATACCAAAT TTTTGAATGT CTTCAGCGAT GAATTCTTGC ATGTATGAGC TGTTTCTCTG      600
TCAATCGCCT TATTGTTTTG ACCAAATCCG ATGACTTTTTT CACCCAGACG TTGTTTGACA      660
ATTTCTTCAA TACCATCAAA AGCACCACCC ACGATGAAGA GGATATTTTT TGTATCCACT      720
TGAATCATCT ACTTGTTGTG GATGTTTGCG TCCACCTTGA GCGGGCACGC TAGCAACAGT      780
TCCCTCAATA ATCTTGAGAA GGGCTTGTG CACCCCTTCA CCAGAAACAT CACGTGTGAT      840
AGACACATTC TCACTCTTCT TGGCAATCTT GTCAATTTC TCCACATAGA TAATGCCACG      900
CTCTGCACGT TCGATGTTAA AGTCAGCAAC CTGCAAGAGT TTGAGGAGTA TATTTTCCAC      960
ATCCTCACCC ACATAACCAG CCTCCGTCAG AG

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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

ATTTTCACAG GGCAGGATGC GGAACGACTA GCCCCATACT TTAACGGAAT TTTGGTAGGG      60
ACAGCTCTTA TGCAGGCAGA AAATGTGGCC CAGAGAATCA AGGAGTTGCA GATTGACAAA      120

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GGTTAAAAATT TGTGGACTAT CGACCAAAGA AGCGGTGGAA ACAGCCGTTT CAGCAGGAGC	180
CGACTATATC GGTTTTGTCT TTGCACCTAG TAAAAGACAG GTGACTTTAG AAGAGGCAGC	240
TGAGTTGGCA AAGCTTATTC CTGCAGATGT GAAAAAGGTT GGAGTATTTG TTTCACCAAG	300
TCGGGTAGAA CTGCTGGAAG CGATTGACAA AGTTGGCTTG GACTTGGTTC AAGTTCACGG	360
TCAGGTGGCA GATGATTTAT TTGAGAAATT GCCTTGTGCC AGTATTCAGG CTGTGCAGGT	420
AGATGGAAAT GGGCATGTCC CCAATTCTCA GGCAGATTAT CTACTCTTTG ATGCCCCCTGT	480
GGCAGGAAGT GGCCAGTCCT TTGATTGGGG TCAACTGGAT ACGACTGGAC TAGCACAGCC	540
CTTCTTTATC GCAGGTGGCC TTAATGAAGA TAATGTAGTA AAAGCAATTC AACATTTTAC	600
TCCCTATGCA GTAGATGTAT CGAGCGGAGT GGAGACAGAT GGACAAAAAG ATCATGAAAA	660
GATTAGAAGA TTTATAGAGA GGGTAAAGCA TGGCATATCA GGAACCAAAT AAAGATGGAT	720
TTTACGGAAA ATTCGGCGGA CGTTTGTGCC CAGAAACATT GATGACAGCA GTTTTGGAGT	780
TGGAGAAGGC CTACCGTGAA AGTCAGGCAG ACCCAAGTTT CCAAGAGGAA TTAAACCAAC	840
TCTTGCGCCA GTACGTAGGA CGTGAACTC CTCTTTACTA CGCAAAAAAC TTGACCCAGC	900
ATATCGGCGG AGCCAAGATT TATCTCAAAC GGGAGACCT TAACCATACA GGAGCCCACA	960
AGATTAACAA TGCCTTAGGA CAAGTTTGGC TTGCCAAACG CATGGGTAAA AAGAAAATTA	1020
TCGCAGAAAC GGGTGCTGGT CAGCACGGTG TGGCAACTGC AACTGCTGCG GCCCTCTTTA	1080
ACATGGAATG TACCATCTAC ATGGGTGAGG AAGATGTCAA ACGCCAAGCC CTCATGTGT	1140
TCCGTATGGA GCTTTTGGGA GCTAAGGTTG AAGCAGTGAC AGATGGTTCG CGCCTGCTCA	1200
AGGATGCGGT CAATGCAGCC CTTGTTTCAT GGGTGGCTAA TATCGACGAT ACCCACTATA	1260
TCCTTGGTTC TGCCTTGGGG CCTCATCCAT TTCCAGAAA	1299

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTTGAATC AACAAACACGT ATCCAAGTAT CAGNATCAAA TTATGCAGGT AATCGTACAA	60
TTGGAAATCA CCGTGGATGG TTCAATCCAA CAACAACCTC TGAAGGTTTT GTTACATATA	120
TTTATGCAGA TTAATTTACA GAGGGACTCG AATAGAGCCC TCTTTTCAGG TTTTACCGTG	180
ACAATCCCTA TTAAAAATTA TATCAAAATA GCTTGAAAAT ATTGGAAAAG TATGGTAGAA	240
TGAAAATTGT CGTGTGAACG ATAATACTCA TTCTTGATGA ATTGTGAAGC AGTTGCCCTT	300
GGGTCGTTTT GCGAGTTGAA GTCAAGAAGA GGAAAAAAC AAAAAGGAGA AATACTCATG	360
GCAGTAATTT CAATGAAACA ACTTCTTGAG GCTGGTGTAC ACTTTGGTCA CCAAACCTCGT	420
CGCTGGAATC CTAAGATGGC TAAGTACATC TTTACTGAAC GTAACGGAAT CCACGTTATC	480
GACTTGCAAC AAACGTGAAA ATACGCTGAC CAAGCATACN ACTTCATGCG TGATGCAGCA	540
GCTAACGATG CAGTTGTATT GTTCGTTGGT ACTAAGAAAA CAAGCAGCTG ATGCAGTTGC	600
TGAAGAAGCA GTACGTTTCAG GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACCTC	660

TACAAACTGG	GGAACAATCC	AAAAACGTAT	CGCTCGTTTG	AAAGAAATTA	AACGTGGATG	720
GAAGAAGATG	GAAC TTTCGA	AGTTCTTCCT	AAGAAAGAAG	TTGCACTTCT	TAACAAACAA	780
CGTGCGCGTC	TTGAAAAATT	CTTGGGCGGT	ATCCGAAGAT	ATGCCTCGTA	CCCCAGATGT	840
GATGTACGTA	GTTGACCCAC	ATAAAGAGCA	AATCGCATGT	TAAAGAAGCT	AAAAAATTGG	900
GAATCCCAGT	TGTAGCGATG	GTTGACACCA	ATACTGATCC	AGATGATATC	GATGTAATCA	960
TCCCAGCTAA	CGATGACGCT	ATCCGTGCTG	TTAAATTGAT	CACAGCTAAA	TTGGCTGACG	1020
CTATTATCGA	AGGACGTCAA	GGTGAGGATG	CAGTAGCCGT	TTGAAGCAGA	ATTTGCAG	1078

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTATGAGGGA	TATAAAGTGA	GAGAGTTGGG	CCAACGTTCC	AAAAACGTCC	TAAATTCTGC	60
CCATTGACAA	AGGCAACCCC	CTTACCAAAC	TCAGACNAGT	CTAGGTAAGT	ATCTTTTGGC	120
TATTCGACTG	TAAAGTCATA	AGCGTAAAAG	GCTGGTTGTC	CTTGAGTCCA	TCCTTTGGAA	180
AAATCAATTT	TCTCAGGATT	GTCTAGTGGG	AGTGGATAGT	GTTTCCAGTT	TAGTAAGAAA	240
TGCAGATCCT	TACAGACCCC	TGTCCGAATT	CCCTTACGTT	GCGTATCCGC	TAAGAACTTA	300
TGCCCATAGT	TGACACGCCC	CATATTTTCT	ATCAAGATAT	CTAACCTAGA	TAGCCCTTTC	360
TTTTTTACCTT	GATAAAAAAT	ATCTTCCCCA	ATCTCTGTCT	GATATTGAGT	TTTAACCCAC	420
TGACCATCGA	CATACAGCTG	GGCCCTATCT	CGACCATCAA	TGATACGAAG	TCTTTCTTCT	480
TCTGCATCCC	AGTTTGTTTC	TGTTTGATAA	AGTAGGTAGC	CATAACTTTG	TCCCAGCTCC	540
TCCATCTTTT	GAGGATAGAG	ACTTTCTACA	GGGACTTGAC	AAGCTATCTA	AGGTTTCAAA	600
CAAAGAACT	TTTTCAACTA	GTGGAATAGC	ATCCAACCTC	ATACTCTCTT	TGTAGAGTGG	660
TTCCAACCTG	GGATACTCTG	AAAAATGTGT	TGCCATCATC	TTCTTGACTG	CAAGATATTT	720
AGCAGTTGGA	TTTCCTTCTT	CATCCAGAAG	GGCATCGTAA	TCATAAGACG	TTAACTTGTG	780
GCAGGTCCAA	ATTCCTCGAG					800

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCACGCAGT TCTGTTACCA AAGACCGTTC AAAAAGCAAA CTAGCAATAC TTATAACTTA	60
TTAGAAATTC CTAATTTTAC CTTGCTAAAC GAATACAGGT CACGATGCCA TCTGAGTCTG	120
TGATTTCCAA TTGGCTCGAT GTCATCCATT TGATTGGTAC GTCAACTTCT TGTGCTCGTT	180
GGGCAATCGT TAACAGTTCT TCTTTATGTG CAACTTCGAT GACATAGTAG GCTAAACCTG	240
GTAAGCCTTG CTTACGCGGA AGCCAGACCT TTTCTTCCC CATTTCGTAA CTGCTAAATG	300
ATGATGGTAA TCTCCAGCCG CAATCCAAT AGCGCCAGGC AACTGAATT TATTCTCTAG	360
CCCTAACACC TTTTGATAAA ACTGGCTGGA CTTTCGACTA TCCTTGACGG AAAGATGAAT	420
ATGCCCCATT CTTGTACCTT CTGCCAGGAT AAAGGGCTCT ACTCTTCCC CCAACTCATA	480
AATGTCCTGC GCCGCAAGAG CCTCCGTCAC TCCGATAATG CGTCCATCTT CTCGAATATC	540
CCATGTGGAA ACTGGCTTAT CTCGATAGAG TTCAATGCCA TTTCCCTCCA AATCTTCCAA	600
GTAATAGCT TCACTGTAAC CATGGTCTGC ACCGCCGACA AGAGGAATTT GCAAATCTGT	660
CAGATGTTTC AAGACATCAG CCAAAGCCTT GCGTGTGGGC AAGAGAATGG CCAAATGGTA	720
AAGACCATAA TGTTCCTCA CTTCTCCGCT CTTCTGTGC TTGAATCAG	769

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTACCCCAAG CCTGCAACTT CCCAAGCTGA TTGGTTGAAT GATTTGTCAT CAACACCACC	60
AGTATCAGTG ACGATTGCTG CTTTTGTCTT CACATCAGAA GATGAAGCTG CGTTACGAGA	120
AGAGCGGTTA CCACATGCAG CAAGTCCAAC TGCTGCCACT GCAACTAGGC CAAGACCTAG	180
CCATTGTTTC TTGTTCAATTA CTGAACCTCC TAAATAAGAT GTGCAACGAT GTTGCAAGTA	240
TGGATTGATT GGTCACAAAG ACCCTTGCCA CTCAAAGAGC GACTCAGACT AATTTAAGTC	300
TGTAAAAGAA TATGGAAGTA ACTCCCCGAC CGTCATCTCG ACCGTCGATT TATCTTTTGC	360
GAATAAGGTC ACTTTTAAAT CTTGTTCAAA AAATTCGACC ATTACTTGGC GACAAGCACC	420
ACATGGTGAA ATCGGTTTTT CAGTTTGACC ATAGACAATC AATTCTGAAA ATTCTCTTTG	480
GCCTTCAGAT ATAGCCTTAA AAATAGCTGT TCTCTCACC CAATTGGTCC AAAGGATAGC	540
TAGCATTTTC GATATTCACCT CCCGTGTTAA ACATTTCCGT CTTTGGCTAC TAAAACTGCT	600
CCGATAGGAA AGTGAGAATA GGGGACATAG GCATGTT	637

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTGAGGATAA	TGACATCTGC	CANAGGAGCA	AAACTAGCAA	AATCATCNGT	TGCACGGTCA	60
ATCATGCCCTT	CTTTCAAGGC	GATATCTCTC	GAAGCTTGAC	TACGGATTAT	AACCTAAAAT	120
TTCATAATCT	GGATGATCGC	GTTTGATACC	AAGTGCCATA	GAGGCTCCAA	TCAACCCAAG	180
ACCTGCGATA	TAGATTGTTT	TTGCCATAGG	AACTCCTTAA	TAGTTCTTTG	TATAGTCTCG	240
GTGTTTGGCT	ACCGCTTCTT	TTAGTTCCTC	AAGATTATCT	GATGAGAATT	TTTCGAGGAT	300
TTCTTGCGCC	AGAACCGTTG	CTACAACGTC	TTCCATGACC	ATTCTGTCAG	CTGGAAGAGC	360
AGTCGGATCA	CTTCTCTCCA	CGGTTGCCTT	GTAAGGTTTCG	TGGGTTTCGA	TATCCACACT	420
CATAAGAGGT	TTATAAAGAG	TAGGAATGGG	TTTCATGACC	CCACGAACAA	CGATGGGTTG	480
CCCATTAGTC	ATACCACCTT	CAAAACCACC	TAGATTATTG	GTACGGCGAG	TATAACCGTC	540
TTCTTTAGAC	CAGAGAATTT	CATCCATAAC	TTGGCTGCCT	TTACGATAAC	CAGCCTCAAA	600
GCCAAGACCA	AATTCCACCC	CTTTAAAGGC	ATTGATAGAG	ACAACAGCTT	GAGCCAATCT	660
TGCATCCAAT	TTTCTATCCC	ATTGGGACAT	AGGAACCAAG	ACCAACTGGG	AACGCCTCCG	720
ACGACTGTCT	CCACAACCCC	ACCGATGGTA	TCACCATCAC	GTTTGATTGG	GTCAATATAG	780
TCCTTGATTT	CCTGTTCTCG	TTCTTGTTTG	ACAATAGAAA	ACTTCCAGAC	TGGGCAGCTC	840
TTTGCTTTAA	TTTCCAGCGA	CTGTCAGATT	TTCCAGGAAC	ATCCATTCCC	TTGCCACCAA	900
AGACCACGAC	ATGGTTGGCA	ATCTCCATAT	CCAGATTTCGA			940

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATTCTACAG	GATCCATTTT	ACTATCTTAC	GCGCCGGGAA	GTAGGCTGAG	ACATAACCAA	60
GTAATAGAGC	CAACAACCTAG	AGTTCCTAAA	ACAGATAAAA	GATTTAATTC	AAAAACCTTA	120
GTGATGGATG	GGTAAAAGTG	ACTTACAATC	GCATTGCGCA	AACTTCCCAC	CCCCTGTGCA	180
ACCAAAAATG	CCAGCAGCAA	GGCGATGCCT	ACAATCCAGA	TAGCCTCGTA	AATAAAAATT	240
CCTTTGACAT	CACGATTCTG	ATAACCAACT	GCTTTCATGA	CACCTATTTT	CTTGAACGT	300
TGCATGATAT	TGATGTAAAT	AATGATACCA	ATCATAACCG	CTGCTACCAC	AATAGCTTGT	360

GATGAAAGCA CAATCAATAA TCCCTGAATA ACACGAATAA AGGTAATCAC AATATCAAGA	420
ACTCTCTGTT AAGAAAGCAC AGTATACTTC TTATTTTCT GTAAATCTTC TGTTACTACT	480
TTTGTCTGTG ATGGATCTTT GAGTTCCAAG ATAAAAAAG ATACAGCTTT CGTAAATCCA	540
GCCTCTTTCA AAATCGTTTC CATTTGATGA GACAGCATGA AACTGTTGCT GTCTCCATG	600
TCATCTTCAT CATTGATTAC ACGTACAATC TTCGTTTGAA ATTGAGCAAT CTTACTAGTT	660
TCGGCAGCAC TTTCTACAAT GCTGACTGAG ACTGATTTGC CAATAAGATC ATTAGCTGTC	720
AAATTTTTTC CTGTCTGTTT ATTCCAATTT TTTAGTAAAG CTGCTTGGA TCGTTAATCC	780
CTGTTTCATT GTATCAGTAT AGAGGGATCC AGCCAACACT TTGTCCGTCT CATTATTACT	840
AACAGAGATA CTTGTATCAT CATAAAGACT CACTACTTGA GCATAAGAAG CATCGTTTGA	900
CTCAAATCCA TTTCTTGCCC ATCTTTTCTT GCCCATCTAT AGTAATATTT GACATGTTCA	960
TCCCNAAAGG ACTCTCCAAA TATNNNATAG	990

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCGGCTAAG ATGCGTGGAG CATCACAAAT TATCCTTATG AGCCGTCATG AAGACGTCAA	60
AAGATGGCTA TGGAGTCAGG TGGCAGACGT GTTGTTCGAG AACGTGGTCA AGAACGAATT	120
ACCAAGGTGC GTGAAATCCT CGGCGGAGGA GCAGACGCAG CACTTGAATG TGTTGGTACG	180
GAGGCTGCTA TAGAACAGGC GCTAGGTGTT CTTCATAATG GAGGGCGTAT GGGCTTTGTA	240
GGAGTCCAC ACTATAATAA TCGTGCTCTT GGTTCGACAT TTATGCAAAA TATCTCTGTA	300
GCAGGTGGGG CAGCTTCTGC TACAACATAC GATAAGCAAT TTTTACTAAA AGCCGTCCTT	360
GATGGTGATA TCAATCCAGG TCGCGTCTTT ACTTCAAGTT ATAACTGGA AGATATCGAC	420
CAAGCCTACA AAGATATGGA TGAACGTAAG ACCATTAAGT CTATGATTGT AATCGAATAA	480
AAAACGAATA GGAGTTTTAG AACTCTATTC GTTTTTATG TTATCCTATT CTTGATTTAA	540
GGTACTTTCT CTTAATGTCA GTCTGGTTCC CAGCATGGTC AGGCTAGGGA TTTCCGACC	600
GTGGAGGACT TCCTTGTTAA GAATATCCAT ACCTGCTCGG CCCATTTCTT CAGTATAAAC	660
TGTAATACTA AGAGAGGGGA GGATAGACCT GTTTGGTCAG ACTAAGTGTC GTTAAAAGGA	720
AAATGAGGCT GACGCGATCT GGCAGGCTGA TTCCAGCTTC TTGGAGGGCA CGGAGGGCAC	780
CGATAGCTAA ACTATCGCTG GCTGCGAAAA ATGCTGGCGG AAGTTGGTCT CCCAAGCTCT	840
GAATGGCCTC CTTCAATTAAG TCATAGCCAG ACTGGGCAGT AAATCTTCCT TGAAAGACCA	900
GTTCATCATG ATAGATTCCC CTCGCTTGAC TGTAGTTTTT GAAGTTTTCT AGACGCTTGT	960
CCTGAATGAT TTCTTCTTGG TCTGTAGTTT CTTCAAGGCC TGTTAGAATC CCGATACGGT	1020
CCATTCCTTG ACTGAGGAAA TAATCGACAA CCTGTTTCAT AGCAGTGTA AAATCCGTGA	1080
TAATACAGGT ATGTCCCAGG GAAAGTGAT CGCTGTCTAG AAATACAAGA GGCTTTTGGT	1140
ATTCTTCAA GGCAGAAATC TGAGCTTCTT GATAGGATTG ATTCTGCTAG GGATAACAGC	1200

CAAAGGCAAT CCTCCCTTTA TCCACCTCAT ATTTGAAACC ATTTGAGCTC TTA

1253

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGTGTACCAT	CAAGAGGCTA	ATTGATGTTT	CTTCCCCCTG	TGCCTCTCTT	GTCAACATTT	60
CTGTTTGAGC	CTTATGCGCC	TGTAATAAGG	CAGCATTCGC	ATCAGCTAAT	CTTCGATTGG	120
CTTTAGAGAA	ATCCCCTTTT	TTTGCTGCCT	GAATAGCCTC	CATAGCATT	CTTTTGGCTT	180
CCCCACCATA	CATAATTAGC	CCCATTACAG	ATTCTAAATT	ACTTTCATCC	ATAACATTCT	240
CCTCAATCTT	AGTCTAATAA	ACTTTCAGCT	AAATCTAAGA	CTTTAGAACC	ATTCATCATT	300
CCATAATCTG	TCATCGGAAT	AACCGCCACA	GGAATCTGTC	TATCTTTTAG	TTTTTCTTGA	360
AAGTCCCCTA	GTAATAGCG	AACTTGAGGA	CCTAAAAGCA	ACACATTTAC	TTCTTTTGTT	420
GCTACAATTT	CTTCTGCTTC	AGGAGCTGGA	ACTGCAAAAA	TTTCTGCATC	CAACCCCTTA	480
TCTTCTGCTG	CCTTTTGCAT	CTTGTCACT	AGCAGACTTG	TACTCATACC	TGCTGCACAT	540
GCTAACATAA	TTGTTACTTT	AGCCATAGCT	TACTCCTTTA	TCACCTATTT	ACTGACCTAG	600
CCAAGCGAGA	TACTGTATGT	CTCACTCCTC	TAATTGCCTT	GCTCAATGCA	TAAATATTAT	660
CGACTGTTGC	CAGTCCCCCA	TATCCTGCGT	CACCTATATG	TTGAATATCA	ACTCCACAAA	720
TTTTATTTCT	AAGTGCAATT	TCCTTAATAG	TATCTGTATC	AGATGTTTCT	TGGCTAGTAC	780
CAATAGCACT	CAATACAAGA	CCACCCTTAC	TATGAACGAG	ATCAACGACT	TCACGCAACT	840
CTTGGTCATG	AAAGGCTGGA	ACGGTTCCAA	CTGCTGGAAC	AAGTATCACA	TCCGCACCTG	900
CTTCCAACAA	TTGCTCTGCG	ACAGAAAGCT	CTGCCACAGG	CTCATTCACT	CCTGCCCCGT	960
GCATCTTACC	TGCAATAATC	AAACCAGAAA	AGTTTTCCTT	AGCAGTTTGA	ACAGCCTTAA	1020
TGATTTCTCG	ATTGCTAACT	CCTGTTCCAG	GATTTCCAGT	CAAACAGACA	AAGTCAAAAC	1080
CTAACTCCTA	TATTCGCTTC	AATGTTTCAA	CACTAGCAAC	ACGACCTGCA	ACAATTTCTT	1140
GTGTTTCCCT	TAGCATTCTT	TGCAGATGGG	TCAATCGGTT	CCAAATTTAC	ACCAATTGGA	1200
CAAGCAACAA	G					1211

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

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CCACACTAGC AGCCTATGGA CTCACTAAAA GAAAAGAAGA CTAAGTCTTT TCGATAAAAA    60
ATAAACAGCG AGATTGAAGC TCGCTGTTTA TTTTAAAT AATCACCTAG TCCAAGACGT    120
TCAAAGATAT CATCCACTCG TTTGGTGTA TAAACTGGGT TGAAGATTTC ATCGATTCT    180
TCTTGTGTGA GACGTGATGT TACTTCTGAA TCTGCCTCAA GAAGTGGTTT AAAGTCTACT    240
TGTTGTGCCC AAGAGTAGGC TGTTTTGGT TGCACCAAGT CATAGGCTTG CTCACGGGTC    300
ATGCCTTTTT CAATCAATGT CAACATAGCC CGTTGGCTAA AGATAAGACC AAAAGTCGAG    360
TTCATGTTTC GGATCATATT TTCTGGGAAG ACTGTCAAGT TCTTGACGAT ATTTCCAAAA    420
CGGTTGAGCA TGTAGTCAAT CAAAATGGTC GTATCTGGTG TGATGATACG CTCAGCTGAT    480
GAGTGAGAAA TATCGCGTTC GTGCCAGAGA GCGACGTTTT CATAAGCCGT AATCATGTGA    540
CCACGAATGA CACGCGCCAG ACCAGTCATA TTTTCAGAAC CGATTGGGTT GCGTTTGTGA    600
GGCATTGCTG AAGACCCTTT TTGCCCTTTA GCAAAGAACT CTTCTACTTC GCGTTGCTCA    660
GATTTTTGTA GACCACGAAT CTCAGTCGCC ATACGTTCTGA TTGAAGTCGC AATGCTGGCA    720
AGAACCGCAA AGTACTCAGC GTGAAGGTCA CGAGGAAGGA CTTGTGTAA AGATTCCCTG    780
GGCACGGATG CCAAGTTTAT CGCAGACATA CTCCTCTACA AATGGTGGGA TATTGGCAAA    840
GTTCCCAACC GCACCAGAAA TCTTACCAGC TTCTACACCA GCAGCCGCAT GCTCGAAGCG    900
CTCCGATATT GCGTTTCATT TCGCTGTACC AAGTTGCTAA TTTAAGGACC AAAGGTTGTC    960
GGCTCAGCGT GCACACCATG AGTTACGCCC CATCATGATG GTGAACCTGT GCTCCTTGGC    1020
TTGTCAGCGA TGATATTAGT GAAGTTTTC AAGTACGAC GGATGATGTC GTTGGCCTGC    1080
TTGTAGAGGT AACCATAAGC AGTATCCACC ACGTCGGTAG AAGTTAACCC ATAGTGAACC    1140
CACTTGCCTT CTTACCAAG AGTCTCAGAA ACCGCACGCG TGAAAGCCAC CACATCGTGG    1200
CGCGTCTCCT GCTCAATTTC CAAAATACGG TCGATGTCAA AGTCCGCCTT CTTGCGAATC    1260
AAAGCCACAT CTTCTTAGG GATTTCCCA ACTCAGCCCA TGCCTCGTCA GAGAGGATTT    1320
CCACCTCAAG CCAAGCACGG TATTTATTTT CTTCACTCCA AATATTCGCC ATCTCAGGGC    1380
GAGAGTAACG GTTGATCATG TGTAAATTTT TCCTTTCTTC TTAAG                    1425

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(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

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CTATTCTGAG TATAAAGTTG GCGGAGGCTG GAACTACGCT CGTTATGAGG TCATAAACTA    60
CTATACTGGA GGTATTAAT CCTTAAAGAG TGAGAAAAGG AGGGCTGGAT ATGTTAAATC    120
TTACTCATGT TACCTTAAAA ACGCGACAAG TCATCTTGCA AGATGCGGAT TTTACCTTTA    180

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AAAAGGGTAG	GATTTATGGC	CTTCTTGCTA	TCAATGGCTC	GGGAAAGACG	ACACTATTCC	240
GAGCTATGAG	CAAGTTGCTT	CCCCTTAGTA	GTGGACACAT	CGCAGTTCCT	CCTTCTTTGT	300
TTTATTATGA	GAGCGTTGAA	TGGCTGGATG	GAAACTTAAG	TGGGATGGAC	TACCTTCGTC	360
TCATAAAAAA	ACATCTGGAA	GTCAGACCTA	AACCTTGAGAG	ATGAAATCGC	CTACTGGGAA	420
ATGGCTGACT	ATATCAGTCT	TCCCATCCGC	AAGTATTCCCT	TAGGGATGAA	GCAACGCTTG	480
GTGATTGCTA	TGTATTTTCT	CAGTCAGGCC	AAATGCTGGC	TCATGGATGA	GATTACAAAT	540
GGCTTAGACG	AGTATTATAG	ACAGAAGTTT	TTTGATAGGC	TAGCACAAAT	CGATAGACAA	600
GAACAGCTGG	TTCTTTTAAG	TTCCCACTAT	AAGGAAGAGT	TGGTTGATAT	CTGCCATAGA	660
GTAGTAACCA	TTCATCAGGG	GCAGATAGAA	GAGGTTTAGT	TTATGAAAGA	TGTTAGTCTA	720
TTTTTATTGA	AAAAAGTTT	CAAAAGTCGT	TTAAACTGGA	TTATCTTACT	TTTATTTGCA	780
TCTGTACTCG	GTGTTACCTT	TTATTTAAAT	AGTCAGACTG	CAAACTCAGT	CAGCTTGAG	840
AGAGAGTTGG	AAACTCGTCT	TGTAGACCGT	GAGAGAGTCA	TCAATGAAAA	TGAAGAGAAA	900
CTCTCCCAAA	TGTCTGATAC	CAGCTCGGAG	GAATACCACT	TTGCTAAAAA	TAATTTAGAC	960
GTGCAAAAAA	ATCTTTTGAC	GCGAAAGACA	GAAATTCTGA	CTTTATTAAA	AGAAGGGCGC	1020
TGGAAAGAGG	CCTACTATCT	GCAGTGGCAA	GATGAAGAGA	AGAATTATGA	ATTTGTATCA	1080
AATGACCCGA	CTGCTAGCTC	TGGCTTAAAA	ATGGGGGTTG	ACCG		1124

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGAGCAACT	TCGTCAAATC	TTCATAGGTG	AGGTAACCAA	TTGGAAAGAG	GTTGGTGGTA	60
AGGACTNACC	CATCTCTGTT	ATCAATCGGG	CAGCCGGCTC	TGGCTCTCGT	GCTACCTTTG	120
ATACTGTCA	TATGGAAGGT	CAGTCTGCCA	TGCAAAGTCA	GGAGCAGGAT	TCAAATGGAG	180
CGGTAAATC	AATCGTATCA	AACAAGTCCA	GGAGCTATCT	CTTATTTATC	TCTTACCTAT	240
ATAGATGATT	CGGTCAAAG	CATGAAGTTG	AATGGCTATG	ACTTAAGTCC	AGAAAAATATA	300
AGTAGCAATA	ATTGACCCTT	GTGGTCTTAT	GAGCATATGT	ATACATTGGG	GCAGCCCAAT	360
GAGTTGGCTG	CAGAATTTCT	CAATTTTGTT	CTCTCGGATG	AGACCCAAGA	AGGGATTGTC	420
AAAGGATTGA	AGTATATTCC	GATTAAGGAA	ATGAAGGTTG	AAAAAGATGC	TGCCGGAAC	480
GTGACAGTGT	TGGAAGGGAG	ACAATAATGA	ATCAAGAAGA	ATTAGCTAAG	AAAATGTTGC	540
TTCCATCAAA	GAATTCTCGT	CTGGAGAAAT	TAGGAAAAGG	TTTGACCTTT	GCCTGTCTTT	600
CTTTGATAGT	CATCCTTG	GCCATGATTT	TGGTTTTCGT	AGCGCAAAAA	GGCTTGTCGA	660
CCTTCTTTGT	CAATGGTGTG	AATATCTTTG	ACTTCTTTT	GGGAGGAACT	TGGAATCCTT	720
CTAGTAAAGA	ATTTGGTGCC	CTTCCTATGA	TTTTGGGTTT	CTTTATCGTT	ACCATCTCT	780
CAGCCCTTAT	CGCAACACCC	TTTGCTATTG	GTGCAGCAGT	TTTTATGACC	GAAGTATCAC	840
CAAAAGGGGC	GAAGATTTTG	CAACCAGCTA	TTGAACTCCT	GGTTGGGATT	CCTTCAGTAG	900

TGTACGGATT TATTGGCTTG CAAGTCGTCG TTCCCTTTGT TCGCAGTGTG TTTGGTGGGA	960
CTGGTTTGG GATTTTGTCA GGGATTTCG TCCTCTTTGT CATGATTTTG CCGACCGTAA	1020
CCTTTATGAC AACGGATAGC TTGCGTGGG TTCCTCCNTT ATTATCGTGA AGCCAGTTTC	1080
GCTATGGGA	1089

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNTNTTAA ACCTTGACCT TANTTGANNA TTATACCGAA ATTNTCTTCA TTTTAAAAG	60
AAAAAGGGC GCTGGTAAAA GGGATAATCT TCACCAACTC CCTATNTTTC TACTTATCTA	120
AGCCTAATTC TGCCAAGATT TGACGTTTGT NGGCAATCTT TNGGACTTCN TNGTCCTCAT	180
CTTCAGACCA GTCTAGTTTA ATTTCTGAAA CAATCTGCCC AGGGNGATTT NTCAAGATAT	240
AGATGCGGTC GCTGAGANTG AGGGCCTCCT CAATACTATG CGTGANGATC AGGTTTGTTA	300
GCTGCAACTG CTTGTGAATC TCAAGATACC AAGCGTGGAG TTCCATCTTT GTCATCTCAT	360
CCAAGGCGCT AAAGGCCTCA TCTAAGAGAA AGAGCTTGTG CCCAAAAAGG TAGGTCCGGA	420
GTAAGGCTAC ACGCTGGCGC ATCCCACCGC TAAGTTCATG AGGATACTTG TCTCTTACAG	480
CTGTCAGCTG GAAGGTCGCA AGAATTTTAT CCGCTCGGGA AATAGCTTCT GCCTTATCCA	540
CCTTTTGAAT CAAGAGGGGC AGAATGATAT TTCCAAGCAC CGTCTTGTGC TCCAAGAGCA	600
GATCCTTTTG CAACATATAA CTCACGTGCC CTTGGGATT TTCTTACCA TCAAGGACAA	660
TTCTCCCTGA CTGAACTTCT AAAATCCCAG CGATTAGATT AAAGAGGGTG GTCTTTCCAA	720
CACCACTTGG GCCTAGGATG GAAACCACTT CGCCTGAAGT CACCTGTAGG TTGATATCCT	780
CTAAATCCT CTCCTGACCA TAGGCATAAC TGACGTGCTC TAGTCTAATT TCTGTCATTA	840
TTTACAAAT TCGTTGGTGA AGCCTTTGTC TGTCAAGTCT TCTTTAAGGA TACCATTTTC	900
TTTATCCCAT TTATAGAAAG CATTCCAGCG AGCTGCGTCA AATTGACCCC ATTTTTCCTT	960
GTCGCTTGCG TATTCTTTTG ACAAGTATTT TTGAGATTCG ATGACAAAGT CACGTTTTTC	1020
CTTGAGTTCA GGTGCATTCT TGATGAGAAT ATCTGCAGCT TCTNCTGGAT GTTCCATGGC	1080
ATATTGGTAG CCTTTTNTGA TGGCTTGGAT GACTTTGCGA GCTTCTTCTT TGTTATCTTT	1140
CAGATAGTCG TTGTTTGCGA TGATAACTGG TGAATATTAN TCAAACCTCT TGACATAGTC	1200
TTTCAANTAC ATGAAGTTAG CATCTACACC TTGAGATTTA GCAAGGATAC CATCCCAACC	1260
GTAGTAAATC CNAGCAGTAT CAAAGACGCC ATTGGCAATC GGTGTGATTG AGTTTGAGTC	1320
NTTANTTGGT ACTNTTTCOA CCTTCTCACA GTCTCCNCCT TGAGATTCTA CCAAGGTTTT	1380
CAACATACNN GTTCANTTGG GTCATTCCAT GTCCCATATT TCTTACCAAC CAAGTCTTTT	1440
GGACTGCCTA CATNTCACA TTACCGAGAG ATGATCCCTG ATGTATTGTG TTCCACCNAT	1500
AG	1502

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

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ACTCTTCAGC GATTTCTTGG CTGAGAATGT CCTCATAGGC AGGGAGTTGG ATGTCCTGAC      60
CATATTTCTT CTTGAGGGCA GTAGTAACTA GGCGATAAGC CAGATTGGCA TTACGAGAGA      120
AGATAGGCCC GNGGAANTAC GAACCAAAGA CATTCTTATA ATGAACCCCT TCACCGACCT      180
TTTCTTCGTT GTTTCATTT CCATAGACAA CCTGTCCCAG CGGTTTTTGG TCATCAGAGA      240
GGAAGGTACG ACCTTGGTGA TTTTCAAATC CATAGTAGGT TTCATCGAAA TCTTTCATTG      300
TGAATCTTGA TGTCACCGAT AAAACGGTTA TTGGTCTGGT TGAGCGTGTA GTGTCCCATG      360
ACCCCTAGCC CTTGATACG TTTTCCTGAA GCTTCAACAT AATATTGACC CAATAGTTGG      420
AAACCACCGC AGATAGCCAG AACTACACCG TCGTTTTGGA TGTAGTTGTC AATGCTCTCT      480
TTTTTAGCAG GTAGGTCGTC TGCAATGATA CTTTGTTCAG AGTCTTGACC ACCACCGAAA      540
AAGGCGATGT CGTAGTGATT TTCATCAAAG TCATCATGGA GAGAAACGAT GTCAACGGTC      600
ACATGGGTTC CCAGTTTTTC AGCCACATAC TTGAGCATGA GGATGTTTCC ATTGTCCTCCG      660
TAGGTATTCA TGAGATTTCC GTAGAGGTGG GCAATGTTGA GCTGATAGGG GTAATTGCCA      720
TCTTTTGAGG AAAGTGAAGT ATAAACCATT AGTTCATCTC CTTTCTAACA ATCTGACGAC      780
TAGCCAGCAG TTCACGAAAT TCCAGCATGG CAGTATAAGT TGCCAGAATA TAGGCATGCT      840
TGCAGTCTTG ATTCTCAATG GTCTTGAGAA CTTGCTCCAG ATTACTCGTT TCAGTGATTT      900
TCTCAGCTGG ATAGCCAGTC ACTCGGAGGC GACGAGCGAT TTCAGAAATGA CGAACACCGC      960
CAGCGTTGAT TTCAGGAATG TCCATGTCAG TGATTTGCTC AAAGTCTGCA TCCCAGATCC     1020
AG                                     1022

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(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

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CCTCCAGGTC TCGGGAACG ACCATGGCCT TTGTTATTGC CAACGAACTG GGAGTCAATC      60

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TTAAGCAGAC	GTCCGGTCCA	GTCATTGAAA	AAGCCGGAGA	TCTGGTAGCT	ATTTTGAATG	120
AGTTAGATCC	TGGGGATGTA	CTTTTATTG	ATGAGATCCA	TCGTTTGCCA	ATGTCAGTGG	180
AAGAGGTGCT	TTATAGTGCT	ATGGAGGACT	TCTACATAGA	TATTATGATT	GGGGCTGGTG	240
AGGGTAGTCG	TAGTGTTTAT	TTGGAGTTAC	CACCTTTTAC	CTTGATTGGT	GCGACGACTC	300
GGGCTGGTAT	GCTCTCCAAT	CCGCTACGGG	CACGTTTGG	GATTACAGGC	CATATGGAGT	360
ATTATGCCCCA	TGCTGACTTG	ACAGAAATTG	TCGAGCGGAC	GGCAGATATT	TTTGAGATGG	420
AAATCACTCA	TGAGGCAGCA	TCTGAGTTGG	CCCTACGTAG	TCGTGGGACC	CCTCGTATTG	480
CCAATCGTCT	CCTCAAGCGC	GTGCGCGATT	TTGCCCAGAT	AATGGGGAAT	GGGGTAATTG	540
ATGATATTAT	TACCGATAAG	GCTTTGACTA	TGCTGGATGT	TGACCATGAA	GGTTTGACT	600
ATGTGGATCA	AAAAATCCTT	CGTACCATGA	TTGAGATGTA	CAGTGAGGA	CCTGTTGGTC	660
TAGGAACCTCT	TTCTGTTGAA	TATCGCCGAA	GAACGTGAGA	CAGTTGAAGA	TATGTATGAG	720
CCTTACTTTG	ATTCAAAAAG	GTTTTATCCA	TGCGGACACC	GTCTGGACG	GGTGGCGACT	780
GCCTAAGGCA	TATGAGCACT	TAGGTTATGA	ATACAGTGAA	AAATAAGCAA	GAAATCCTTA	840
GAGGCTTTTT	AGAGAAAATC	CAGATATGAT	GGCCATTCTG	ACGATCATCC	GAGACCTTGG	900
TCTGAAAGAC	TCGTGGTTGG	CAGCAGGTTT	TGTCAGAAAT	TTCATTTGGA	ATCTTTTGTC	960
AGACAAATCC	CCTTTTGATC	ATGAAACAGA	TATAGATGTT	GATTTTCTTT	GATCCCAGAT	1020
TTTTCTTATG	AGGAAACCTT	ATTACTGGAG	AAAAAGCTGT	GAGAGGATTT	TCCTCAGTAC	1080
CAGTGGAAT	TGAAAAATCA	GGTCTATATG	CATCAGCACA	GTCCTCACAC	TGCTTCCTAT	1140
ACCAATTCTC	GTGATGCTAT	GAGTAAGTAT	CCAGAACGGT	GTACGACAGT	TGGACTGCGC	1200
TTGAATGAAG	AATCAGATTT	TGAACTCTAT	GCACCTTATG	GTTTGGAGGA	TATTTTGAAT	1260
TTCAAGTTTCG	TCCAACCTCT	CATTCTTAG	AAAATGAAGA	CCGAATGGAA	CTCTATCAA	1320
CACGTTTATC	CAAGAAAAAT	TGGCAGGAGA	AAT			1353

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTCCTGGA	TTCTGGCAAG	TAGGCTGGAT	GAATGTTGAC	AATCCGACCT	TCATAAGCCG	60
ACAATAAGGT	TGGTCCAACG	ATTTTCATGT	AGCCTGCTAG	GCAAACCAAG	TCAATCTGGT	120
GTTCTTCCAA	GAGTTCGACA	AGGGCTGCTT	CGTAGTCTGT	CTTGCTCTCA	AACTCCTTGA	180
GTTCAAAAGC	ATAGGACAGA	ACGCCGAGCT	GCTTTGCACG	CTCAAGCACA	TAGGCATCAC	240
GATGGTCTGA	AAAGACAAAC	TCCACTGGAA	ATCTTTCGGC	AATCACCTGA	AAATTGAGC	300
CATTACCAGA	GGCAAAAACC	GCTATTTTTT	TCATTTGATA	ATGACACTTT	CGTTTTCTTT	360
CTTGACGATG	CGACCAATTT	CATAGACTGC	TTCATCCAAC	AATTCTTTTA	CACGCTCTAC	420
ATTTTCAGGG	CTGACCGCCA	ACATAAGTCC	CACACCCATA	TTGAAGATTT	CAAACATTTT	480
TTCGTGTTTA	ATCTGACCAT	ATTTTTCAAG	GGCTTTGAAA	ATTGGAAGCA	CTGGAACTTT	540

GCTTTCATCA ATTTCAGCAG

560

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

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CTTCAACACT TTATTTTAT CTTTCTCCCA TTTCGTATGC TAGTTCGGAA ATTGTTGCTA    60
GAACCTCTCC GACTATTTGG GATGTTCTCA TTGCTTTTGT AGGAGGGATA GCAGGTATTA    120
TTGGTGTAGT GAAAAAAGAG ACCAATAATA TTGTTCTCTG TGTTGCTATT GCAACCGCCT    180
TGATGCCTCC TCTTTGTACA GTAGGTTATG CTATTGCTTC TGCTAATCTA AAATTTATCA    240
TTAGGCTCCT CTTACCTATT CCTCATCAAT TGTAGCTTTA TTGTCATTGC GACTTATATA    300
GGTGTTAGGT TGATGATGGT TAAGAAACAT TATTTTAAAG ATAATGAAGA AGACTCTAAA    360
ATGCGTAGGA TTTTGCTTCT AGTTGCTGTT TTGCTGATGA TTCCGAGTTT CATCTCTGCA    420
ACGACTTTAG TGAGAGAAAC GTTGAAAAAA GAGTCCCTTA AGAAATTTAT ATCAGAGCAG    480
TTTCAGGGGC ATAATATTTT GAAAAAACC TATTCTAAAA AGACTCATAC CCTAAAGCTA    540
ACCATTTTCA GAAATTATTT GACAGAAGAA GAACTCGATA TGATTTCAAG TAAGAGAGGT    600
GACTATGGTT TAAGTGATGT TTCTGTTCAA GTTTCACAAT TGTCTGATTC AGAACAACTT    660
AGTAAGGAAG AACTGGTGGA GTATTTCTTC CAGTATATCA AGGATAAGGA AGCAAAAGAA    720
AAGGAAAAAG CTAATAAGTT TTATACAGAG TCTGAGGAGC AATAATTTCT TGAGAATAGC    780
TGGTTTTTCT CGTGAGTCTT CTATGTATAT CAAAGGAAGA CTGAGGTTTT AAGTATGAAA    840
CTTTTCTTCT ATTATAGTAG                                     860

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(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

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TCTTGGCCAA CTGCATGGAG TTCAGCGGTC AATTTCAACG CACCTGAGAA ACAGACCCCT    60
GCACCCCTGA AATCTCAGGA GACATGATGG TCTGGATGGA ATCAATAATG AGAAAGTCTG    120

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GCTGGATACG CTACCACTTC TGCACGAACA CTCTGCATAT TGGTCTCTGC ATAGAGATAA	180
AACTCACTAT CAAAATCACC TAAGCGCTCT GCACGTAGTT TAATCTGCTG GGCAGACTCC	240
TCCCCACTGA CATAGAGAAC TGTCCCCACT TGGGACAAC TGGTTGAGAC TTGTAGGAGA	300
AGAGTTGATT TCCCAATCCC AGGATCCCCA CCGATGAGGA CGAGACTTTC CTGGTACAAC	360
TCCGCCTCCA AGCACACGGT TGAATTCCTC CATCTCCGTC TTGGTTGAT TGACATTGAT	420
GGAAGTCACC TCAGCTAGTT TCATGGGCTT GGTTCCTCA CCTGTCAAGG ACACACGCGC	480
ATTCTTGACC TCGGCAACCT CAACCTCTTC CACAAAAGAA GACCAAGACC CACAGTTGGG	540
GCAACGTCCC AGATATTTAG GGGAATTATA CCCACAATT TGACATACAA ATGTCGCTTT	600
TTTCTTTGCG ATGACAAACC TCTTCTATA TCTCTAACTC AACTCAATC ACTTGGCAAA	660
AATCAATCTT CTCATTGGC ACAACTGGC GCATGAGCAT TCGATGAGCA ACAACTACCA	720
CAGTCTGATG TTCTCGATAC TTAAACATAC ATTCTAGAAA CCGAGACTTC ATTTCCGTAG	780
CTGTCTCATA TTGAATAGGA CTATTAGGAA GCAACTCCCC CTTGTTTTCT AAAACAGTC	840
TTCTAGCTGT TTCAAAGTTT TCTATTCCTG TTTTATAGAC CTGCCATTCA TGTAATAAAG	900
GCTCTACTCT TAAAGGAAGA CCCGT	925

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTCTNGATCA AGTCAAGGAC TGCANGCCAC GACCGACATA GCGTTTGGCA ATGGAAACAA	60
CCAAACGAAG ATTGGCTTCC GCAAGACGTT GTTTGGCTTC GATATCGCCA GCTTCAACAG	120
CCAGTGCCAA CTCTTCTCC TCTTCATTGG TCAAGAGAGG AACGACCCCT ATTTCTTTCA	180
AGTACATACG GACAGGGTCA TTGACCTTAG CAGAAGTTGA CCCAATCAAG TCCTCATCGC	240
TGAGTTCTGG TTCTTCTTCA TTGCTAAGAA CACGCGCACT TGGATTTCCT TCGTTATCTG	300
TGATAGAAAT GCCTGCATCC TGAATCCGTT GCAAGAGATC TTCAATCCCA TCAGCGTCCA	360
AGGTAAAAGG AATAACCAGA CTTGCATTGA TTTCATCATC TGTGCTGTC CCTTTTGTCT	420
TATGATTACG GATAAATTCT GCTACCTGTA CGTCAAATGT TGTACTTCT TTTTGTTTTG	480
TTGCCATTAT TACTCCATTC TTCTCTTTTG GGAAATTAAA CGTTCCAATT CTTCTAGGGC	540
TGTATCTGTA TCTCCTACAT GGCTAGCTTC CTGCACCTTC TTTTGTATT CCATATTGTC	600
CTGATTCAAG AGAGCCTTGT TTCGAAGTCA	630

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTAGGGCCAT	CTTCTCACCT	CCTCCTTGTC	AGTACATTCT	TGCAATAGAA	AAAATAAGAT	60
TGAGTCCCC	CAACCTTAAA	TTTTTTCACC	ATCTTCTTTT	TCTTTAGCAA	TTTGCTCTTT	120
GATTTTCTTT	TCTTCTTCTT	CTTTGCGGCG	TTTTTCTTCT	TCGATACGGC	GACGCACTGC	180
TTCACGTTTT	CCTTCTGGAT	CTGGGTGAAT	TGTAACGTTT	CCTGATTCTGA	TTTCTTCTAA	240
AGCGCGAAGA	GTTGATTTTT	CAGACTTGAA	ACCTTGAGTT	GCTGGGGCAC	CTGCTTCCAA	300
TTCGTGGGCA	CGTTTTGCTT	CCAAGATTAC	GAGTGAATAT	TTTGAAGGAA	CCTTGTCGAG	360
CAAGGTATCA	ATAGAGGGTT	TTAACATCAT	TTGCTTGTA	CTATTTTCTA	AATTTTATCG	420
GGTAGTTGGA	GATTTTGGTA	ACATCTCCTG	ATAGTGACCA	ATGACACGAT	CCACACAGAA	480
GTGTTCTGCT	TCAATCACAC	ATTGACACG	TTCAGCAGCT	AGGGGTACCT	GATCGTTGAC	540
AATCGCATAA	TCATACTCAC	GCATGAGGGC	AATTTCTTCC	TTGGCCTTTT	CGATTTCGTTG	600
GGCAATCACT	TCTGCACTAT	CTGTTCACG	ACCTACCAAG	CGTTCCTTGA	ATTTCATCCAA	660
ATCTGGTGGT	GTCAGGAAGA	TAAAGACAGC	ATCTGGAACC	TTTTTCTTGA	CCTGAAGAGC	720
ACCCTGAACT	TCAATTTCAA	GGAAAACATC	GATTCCCTTG	TCCAAGGTTT	CATTGACATA	780
GGTCAGAGGA	GTTCCATAGT	AGTTGCCGAC	ATATTCTGCG	TATTCCAACA	TCTGTCCTTG	840
ACGAATCAG						849

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCCAAACAAC	GCATCCATAA	TGGTTAAATC	TTGATAAGGC	AGAGCTACAT	TCAAAACAGC	60
TTGCTGGTTT	GTAGGCTTTC	AATCAGAGCA	ATCACTTCTT	CAACCTTGTC	AGCATCAAGA	120
GCAGCTGTCT	CAATCTTTGT	ACTTGTTTTG	CCTTCCAGTT	TAGCTTTCAA	GTCATCGCAT	180
TTTGACTTGG	TACGGCTAGC	AATCATAATC	TCTGTAAATG	TTTCGCTATC	TTGACAAATC	240
TTTGAAATAG	CAACTTGGGC	AACGCCCCCA	CAACCAATAA	CTAGTAAACG	ACTCATTTTT	300
TTCTTCCCTC	TTCTTCTAAA	ATGTCTCAA	CATACTTGGG	CAACATAAAG	GCTCCCACGT	360
GTAAGTTTGC	AGTGTAGTAT	TCTGTGAAAA	GCTGGCGTTT	TTTCCAGCCT	TCCTTGTCAA	420
AATCTTTGAC	AGGGTGGTAT	TTTTTCGATG	CAAATCCAAA	CAACCAATAG	CCAGCTGGGC	480
TAGTTGGAAT	ATGGGCCTGA	TAAACCCGAC	TGATTGGAAA	GGCTTGATTG	ACCTTGCGGT	540

GCATGCTTCG GCAGGCCGAC TCATCCTCGT CAAAGAAAGG A

581

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTCTGAAAAT	CCATACTTCT	ACCAAGGAGA	TACGCTAGCG	GTCTCGGAAG	TTCTCATACT	60
TCTATCGCTA	TATCTGGCCA	TCGCCTTTCT	ATCCAAGGAT	TGACAACAAG	AGATAAGGCA	120
GAGAAAAAAT	TCTTGCTGGA	TCAGCTGGTT	GCCTGCGATG	GTGGTACAGG	TGTCATGCAC	180
GAAAGCTTCC	ATGTAGATGA	TCCGACCCTC	TACTCTCGTG	AATGGTTCTC	CTGGGCTAAC	240
ATGATGTTCT	GTGAGTTGGT	CTTGGATTAC	TGGATATTC	GCTAAGGGGC	TCGCTTTAGC	300
TCAACCGATT	CTTATCAGAA	TCACAAGTTT	ACATTTAAAA	CGTTAAAATT	TAAATTTAGA	360
ATGAGGTTTT	ACTTCATGGA	AAATGTTGTT	GTACATATTA	TCTCACATAG	CCACTGGGAT	420
CGTGAGTGGT	ACTTGCCTTT	TGAAAGCCAT	CGTATGCAAT	TGGTGGAATT	GTTTGACAAT	480
CTCTTTGATC	TCTTTGAAAA	TGACCCTGAG	TTCAAGAGTT	TCCACTTGGA	TGGACAAACT	540
ATTGTCCTTG	ACGACTAACT	TACAAATTCG	CCCTGAAAAT	CGCGACAAGG	TCCAACGCTA	600
CATTGACGAG	GGCAAGCTTA	AAATTGGTCC	CTTTTACATC	TTGCAGGATG	ATTATTTGAT	660
CTCCAGTGAA	GCCAATGTCC	GCAATACCTT	GATTGGTCAA	CAAGAAGCTG	CCAAATGGGG	720
TAAATCAACC	CAGATTGGCT	ACTTTCAGAG	TACCTTTGGA	AATATGGGAC	AAGCGCCTCA	780
AATTCTTCAA	AAATCAGGCA	TTCACGTGGC	GGCCTTTGGT	CGTGGTGTGA	AGCCGATTGG	840
ATTTGACAAC	CAAGTCCTTG	AAGATGAGCA	GTTTACGTCT	CAGTTTTCAG	AAATGTACTG	900
GCAGGGTGTG	GATGGTAGTC	GTGTTTtagg	TATTCTCTTT	GCCAACTGGT	ACAGTAACGG	960
GAATGAAATT	CCAGTTGACA	AAGATGAGGC	CTTGACCTTC	TGGAAACAAA	AATTGTCAGA	1020
TGTGCGTTGC	CTACGCTTCG	ACCAACCAAT	GGTTGATGAT	GAAACGGCTG	TGAACACCAG	1080
CCTGTCCCAA	AAAAAATCTG	AGCGAAGCCA	TTCCGTGTGG	CAAATGAACT	CTTCCCGGAT	1140
GTAATCTTTG	TTCATAGTTC	TTTGTATGAA	TATGTTCAAG			1180

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTCAAAAAGT	CTGAAATTGG	ATCATTTGGA	ACCATCTGAG	CAGTAAGTTT	AACACCTTTT	60
TCTGCCAGTT	TGTGGAAGTC	TTCCACATCC	TTGTCTACTA	CGTTGATAGA	ACGTGTAATA	120
GAACGAGTTT	CTGGTGTTTG	AGACATATTC	CCAACATTAA	GGGTTTCAAG	TGGTACACCT	180
GCTTCTACCA	AACCAAGGGA	AGCGGTCTGG	TTTACGAGCC	ACGATAAAGA	GACGTTGGCT	240
ATCGTATTTG	CCAGCAAGAA	TATTGGCTGC	AGCTTTCTCA	ACTGGCAAAA	TACTCAATTT	300
CACACCTGGT	GGTGTGCGAA	GTTTCAAACC	ACTCTTTTCA	ATATCGTTGT	TGACAACCTC	360
GTCGTCTACA	ACCATAATGC	GTGAAACATT	TAGTTTTCCA	GCCCAAAGAT	TGGCTACTTG	420
TCCGTGGATC	AAACGTCCAT	CAATACGGCA	TCCTACAATT	GTCATAAGTT	TTCCCCCTTT	480
ATATGTTTTA	GTGTAGGTTT	ACGAGTTAAA	TGAATCTCTT	CTTTATATTG	ACCTTCTGTT	540
TCAAAGATAA	TGATGCGGTT	GGCACCTTCC	TTGAGATAG			579

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGCATANCCT	AAAAGTTTTT	TTTGACATCT	TCTGGAATAT	CTGTATCATT	AGCTTCCTGA	60
ACATCTCTAC	CATAAATCCC	AAAGGCTGGA	ATCCCTTTTT	GAGCATGTGA	AGCTAGTACA	120
GCTGCAAGAT	AGACAGCTCC	TGGGCGTTCT	GTCCCATTA	ATCCCCAAAT	AGCATGAGGA	180
ATATCTGGAG	ACATATCCAT	AGTTTCACTA	CCATAACACC	AGCATGGTGT	AACTGTAATT	240
GTTGCGCAAA	CATTTGATTT	TTTAAACAAC	TCATGGGAAG	CTGCAGCCTC	TGGAACACGA	300
CCAATGGTAG	ATGGAGAAAT	CACACATTCC	ACAGGTTCCT	CATCTGGATA	TTTCAATGTG	360
CTTGAAATCA	AATCTGCCAC	ACTTTTAGCC	ATGTTTCATT	TTTGTACTTC	AAGTGATTCT	420
CGTACACCTT	GACGACGACC	ATCAATAGTC	GGACGAATCC	CAATACGTGG	ATGTTGAATC	480
ATACTATTTT	CCTCTTATTT	TTCTGTTTCT	TTCATACTAC	CATCGCCATT	ATATTTACGG	540
TAGCCTGGGT	GACGACCTGT	AACCTTATAA	TTTTCTCGCA	TTGAGAATAG	ACGTTCTAAA	600
GTCGGACGAG	CAATTTCTTG	CTCCTCAATG	CCCTTTGTAG	AAAGTAACAT	TCTTCCGTGG	660
AAGGTTGTCT	TTGCGACTAA	TTCTAAAGTT	TCCATACGGT	AGTATGCTGT	AATTACATCG	720
CTTCCGACAG	TCAGAG					736

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCATTGTAT TTAGGAGAAA TGATGGTATC TTCCAAATCA AAATCAACTT CACTCCATAG	60
TCTCAACGGA TTGATTTTCC CATCTTGATA GGTACATCC TTGTCAAGGA TAACTGAGT	120
CAACGCCTCA TGCTGACCTT GACACCTGAT GTCATCTACC AAGAGCCAGA CATCCTCTAC	180
CAACATGAGG ATTTTCTCT TGTGAAGATA AGGCAAATCA GGTCTGCTG ACCAATAAGC	240
CCCTTCAATA TAATGCATTC CCTCCCTTTC TTTATGGTGA CAAAACAGGG AGTGAGGATA	300
GTATTCATAT TCCCAGGATC CCGTGATTCT TTCCGGAGCT TTCCCATCTA CAATGCAGGT	360
CGAATGACTC CAAGCACTCT TTAAGAGATA ACGTTTCATAT ATCTCCCGAT AAGAATAACG	420
CCCAGCATCT ATGAAAATAG GTTGGCCTTG ATACTGTAAG CAAAACATAT TCTCGTCACT	480
ATGGCTATGG GCACTTCCTA GCGGACCATT TTTGAAAAAT AGATAACGAT GTTCATCCTT	540
AATGCAGACA TGTCCAGAGT CTTCAAAGAT CATGGACTTA GGCTGCCAAG	590

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAGTGTAGC TTCCTTAATC TTATCTGATA AGATAGCTGT CATATCAGAC TCAATCATTT	60
CCTGGAGCAA TCACATTGAC TCGTATATTC CGACTAGCGA CCTCGCGTGC CACAGACTTG	120
GTAAAGCCAA TCAAGCCAGC CTTAGAAGCA GCATAGTTAG CTTGACCAAT ATTCCCCATC	180
AAACCAACAA CACTAGACAT ATTAATGATA GCACCTTCTC TGGCTTTCAA TCATCGGTTT	240
CCAAAGACTG ATTGTGTCAT ATTAAAGGCA CCAGTCAGAT TGACCTTGAG CACTTTTTCA	300
AAATCTGCTT CTGTCATCTT GAGCATAAGA GTATCTTGGG TAATCCCTGC ATTGTTGACC	360
AAAACATCTA CTGAACCCAG TTCTGCAATA GCTTGATCAA TCATACGCTT AGCGTCTGCA	420
AAATCTGATA CATCTCCTGA AATGGGAACC ACCTTGATAC CATAGTTTGA AAATCAGCG	480
AGCAATTCTT CTGAGATTGC CCCACGACTG TTAAAGACAA TGTTGGCTCC TGCTTGAGCA	540
AACTTGTGGG CGATGGCAAG ACCAATTCCA CGACTCGAAC CTGTAATAAA GATATTTTGA	600
TGTTCTAGTT TCATTTTTTT CCTTCAAAA CTCTACTTA TTTTAGTCTA TTTTCTAAA	660
AGTGCTACTA AACTCGCTTG ATCTCCACA TGAGCTAAGT GAGCAGTTTG ATCAATTTTT	720
TTAACAAAAC CTGACAAGAC TTTCCCGGT CCAATCTCGA ATAAAGTTGC TTATGCCTGC	780

TTCTTGACATG	ACCCCAATAC	TTTCATAGAA	ACGAACGGGT	TCCTTGACCT	GACGCGTCAA	840
GAGCTGAGCA	ATGTCCTCTT	TTTGCATCAC	AGCAGCTTCT	GTATTGCCGA	CTAGGGGACA	900
AGTAAATCT	GAAAACTTA	CCTGAGCTAG	AGTTTCAGCT	AGTTTCTGGC	TAGCAGGCTC	960
AAGGAGAGCG	GTGTGAAAGG	GACCTGACAC	CTTAAGAGGA	ATCAAGCGTT	TGGCACCTGC	1020
TTCTTGCAAA	AGTTCAACCG	CTCGATCAAC	TGCAACCACT	TCTCCAGCAA	TGACGATTTG	1080
TGCAGGTGTG	TTATAGTTGG	CTGGAGTAAC	CACTCCAAGT	TCCAGAAGCT	TTTTGACAGG	1140
CTTCTTCAAT	GACCTCTACT	GGCGTATTGA	GAAGTGCTAC	CATCTTGCCA	AGTTCAGCA	1199

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTACTATTTT	CTTTGCCATA	GCCTTCTCCT	TTACACACTA	CGCATATCGT	GGTAAGAAAC	60
ACTGCGTCCC	ATCTCACCTG	CATTCTCTTT	TTGAACAAAG	GTATTAGCGT	TTATATAGGC	120
AATAGCAGAA	GCCTTCAACA	CATCAAAATC	AAGCCCTGCT	GCATTAAAGA	TGGTTTCTGT	180
ATCCCTGTTT	TCAACAGTGA	CCAACAACCC	GATCCTGGGC	ATCGATTCCA	TCTGTTACCG	240
CATTGATAGT	GTAGGACACC	AAACGAACAG	ATTGGTTAAA	GAACTTATCG	ATAGCGTTAA	300
AGATTGCTTC	AACGGAACCC	TGTCCCTGTC	GCATTAAATT	CGACTTTCTC	ACCATCCATA	360
TTGGCTAGGC	TAACGAGCGC	TTCAATGTCA	TTATCTGCAT	GAGTTTGAAG	TTGTAAATCA	420
TCAAAGTGGA	AGCCTTCTGG	ATTTTCAACC	ATGGTTCCAG	CTACCAAAGC	TCGAGTATCT	480
GCATCTGTGA	TTTCTTACTT	CCTATCGGCC	AGTGCCTTGA	ACTTAGCAAA	GAATGGTTTG	540
ATATCCTCTT	CTGTAAAATC	TAAGGCCAAT	TCTCTCAGTT	TCTCAACAAA	AGCATGGCGA	600
CCAGATAATT	TTCCAAGCGG	AATCTTAACA	CCAACCAATT	CAGGTGTGAT	GATCTCATAA	660
GTGAGAGGAT	TTTTAAGGAC	TCCATCTTGG	TGAATACCAG	ATTCGTGGGA	GAAGGTATTG	720
CCACCAACGA	CGGCTTTGTT	TTTAGGAACT	GGAATACCAG	AGAAGCGAGA	AACCATTTCT	780
GACGTATTGA	TGGTCTCATT	TAGGACAATA	CTGGTTTCTA	CTTGGTAGTA	ATCTTGCGCA	840
ATATTGAGAG	CCACTGCAAT	TTCTTCCAAA	GCAGCATTTT	CAGCTCGCTC	CCTAATACCA	900
TGGATAGTCT	CTTCAAAAAG	TCCTGCACCA	TTCTTGACAG	CAGCAAGGCT	ATTTGCCACT	960
GCCATCCGAA	GTTTCATCATG	ACAGGGAGGC	GAATAGATGA	TCTGACGATC	CGTCTGGACA	1020
TTCTCAATCA	GGTATTGGAA	GATGGCACCA	CATTCCTCTG	GTGTGGTAAA	TCCTATATTT	1080
TCTGAAAATT	TCTTCAGTAA	AGAATATTTA	GCTAATTGAA	AGTTCATGAA	AATTATTAAA	1140
ATATTTCATT	TTTTAGAGGT	TAAGTTCCAA	CTTTTTTCTA	TCAATTCCAG	TACTTNTTCA	1200
TCTGATAAAG	TATCATCAAG	GGACACACTA	ATCCAGTAGC	GCTTGCTCAT	ATGGAAGGCT	1260
GGATAAATCC	CCTTTTGTGA	AAGCAAATTA	GCTACTTGGT	CATGCTTGAG	GTTGACTGCT	1320
TCCACTTGTC	CTTCTCTGCC	CTTTTCCAGC	TTATTCCAAG	AGATTTTCAN	CAAGACGGCA	1380
TACCACTTTT	GATTGCCTTC	ATGGCGCAAT	ACAG			1414

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

CTCCCCATTT TGGAAAATTT CTGTCAAGAA ACGGCGAACC AGCTTTTAT TTTCTGCTTT      60
CTTGTCCTAAA TCCTTGATTT CAAAATCTCC AAAAATTTGA TCTAGTTGGT CATTTTCAGG      120
TGTTTCGATAG TAGTCAATGA CATCCCAATG CTCAACAATA CGACCATTCT CATCCGCACG      180
GAAAGTATCC GTCGTCACCC ATTGAGCTTC TCCACCATTG AGATATTGAT GGAACATGAA      240
CAAAGACCAG ATTGCCATCC TCAATGGTGC GGACAATCTT AATCTGACGC TCTGGATGAC      300
GCTCAAAGAA ATCTGCAAAG AAGGCTGCAA ATCCTTCTTT CCCGTCAGGA ACACCTGTCTG      360
AATGTTGGAT ATAGGTATCC CCTACAGACT GGGCTTGAGC CTCAGCAACT CGTCCGTCTT      420
GAATGGCATG GATGTATAGG TTGTGAGCAT TTTTCACTTG TTGTGACATA TTCTAAACCT      480
CATTTCCCTT CTCTTTCAGA TTCGCCAAAA TTCTTTCTTG AAAACCTTCA AATTGGTGAA      540
TTTCTTCCTC TGAAAATCCT TTGTAAAAGA TAGTATCCAA TTTCTGACTG ACACGATGCC      600
CCACTTCTTT CTGGGACTTG CCTAACTCCG TTAAACTAA ATACTTCTTA CGCTTGCTCTT      660
TTCCACACGG ACTAACAATT ACAAGCTTTT GTTCCTCTAG CTTTTTTATC ATAGTCGTCA      720
CGTATTATT CGCAAGCCCA GTCGCAAGCG                                         750

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(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

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GTATCGTTCA ATTCCAAAGA TACGGAGGAA GCTGCGTTTC GCGAGAAAAC TCTTGTTAGA      60
CCAGATAGGG ATTAGCCAAA ATCCTTCTAT GNGCTTATAT CCAAATGGAG ATGCAAACCT      120
CTGCCCAACT CTTGACCAAT AAGATCTTTC TTAATAATCC ACTCAAGGCT CTGGTAGAGG      180
AAAAATATGG GATTGAGTAT GAAGAATTTA CCAATCCTTG GCACGCTGCC ATTTCTAGCT      240
TCGTTGCCTT TTTCTTAGA AGTTTGCCTC CAATGCTGTC AGTGACCATA TTCCCAAGTG      300

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AATATCGCAT	CCCTGCTACT	GTCCTTATTG	TCGGTGTGGC	CCTTCTTCTC	ACTGGTTACA	360
CTAGTGCCAG	ACTTGGAAG	GATCCGACTA	GAACAGCTAT	GATTCGGAAC	CTTGCTATTG	420
GTCTCTTGAC	CATGGGAGTT	ACCTTCCTGC	TCGAACAAC	TTTCAGCATT	TAGAATACAA	480
GAAATACCTC	GATTTTGAAG	TCGAGGTATC	TTTTTTACAT	TTGCACAATC	TTGCGATAAC	540
TTCTTGAACT	AATCATGAAA	ATCAGCACAT	AGGCGATGAG	GAAGATAGCG	CAGATAGACA	600
AGGTCACAAT	CAACATCATA	GTCGTATCCA	GTACACCAAT	CACTTTTAAA	ATCAGGCTAA	660
GCATATGGTA	GGCAAAGGCG	AGATGTATGA	AGGCAAAGAG	CAAAGGAAGG	AAGAAAACAG	720
TTAAAACCTG	TTTGTGATG	GTTTGCTTGA	TTTGCTTTTG	GTCCAAACCG	ACTTTCTGCA	780
AGATAATAAA	GCGTTCACGG	TCTTCGTAGC	CTTCAGAAAT	TTGTTTGTAG	TAGATGACCA	840
GAACAGTTCC	GACCATAAAG	ATAATGGATA	GGAAAATACC	GATAAAGAAG	ACACCGCCAA	900
AGAGGACACT	CATTTGAGCA	CTAGCATCTG	CTAGATTGCT	ACCATAAACA	TAG	953

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGATTGAAC	TTCTATTTAC	TAATATTCAA	AAATCCTCCG	TTTCAAAGAG	CAGGGAAGTC	60
TTTGTGACAG	AGGATTTTTT	CTATAGGGCT	TTAGCAGCTG	CAATTGCGGC	TTCGAAGTTT	120
GGCTCAGAAT	TGATATTATC	CACGTATTCA	ACGTAGCGAA	TCGTATTGTC	AGTATCGAGG	180
ACAAAGACTG	CGCGTGCTAA	TAGGTGCCAT	TCGTTGATCA	AGAGGGCATA	ATCGCGCCCG	240
AAAGAATGGT	CAAAGTAGTC	TGAAAGCATA	ATGGCATTGT	CAAGGCCTTC	AGCACCGCAC	300
CAACGTTTTT	GAGCAAAAGG	TAGGTCCATT	GAAACAGTCA	ATACGACCGT	GTTGTCCAGT	360
CCAGCCAATT	CTTCATTAAA	ACGACGTGTT	TGAGTTGAGC	AGATGCCTGT	ATCGATAGAA	420
GGAACGACAC	TCAAGACTTT	TTTCTTGCCA	TCAAATCAG	CCAGAGATTT	TTTAGAAAGA	480
TCTGTTGTAG	TAAGAGAAAA	ATCAAGCGCC	TTGTCGCCGA	CTTGTAGTTG	TTTACCTGTA	540
AAGCTCACAG	GATTTCCGAG	AAAAGTTACC	ATAGGATACT	CCAATCTTTT	TTCTTCCATT	600
GTATCTGAAA	CAGTCAGAAT	TTTCCAATGA	TTTGACCGGA	AATGTGGGCA	TAGAAAAAAC	660
GCCAG						665

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

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CTAAGTATAA AAAACTTGCC GAAAGTATCT CTGAAGTTAA TTTGAATGTC TTTTTCAAA    60
ATGCTTTAGA TTTTGTTGAA ATCTTTAATC AAGAGCCTTG TCTGATAAAT TTTTGTGAGT   120
TTATGAATTC TATGTTACAA GGCGATATTC CAAAGTTAAC AATAAACCAA GAATAATAAG   180
AGGGGAACAG TATGAAAGAT ACGATTCTTA ATAAGGATTT GATTTCATG GGCTATAGAC   240
CATCAACAGC AAATGCTATT ATCCATCAGG TGAGAGAATT ACTTGTATCA CGAGGCTATA   300
CATTTTATAA TCGCAAACGT TTGATGGTTG TTCCAAAAG TGTGTGAAA GAGTTGTTGG   360
GAATGGAATT GTGAAATGGC TTATATCGAG TATAAACAGC GTGGGAAGAA AAGGCTTTGG   420
TCGTTTTCTA TACGTGAGAG GAGCAAGAGC CTACTCCATA AAAGCGGATT TAAAACAAAA   480
CGAGAAGCTA AAATAGAAGC GGAGAAAGTT CTTCATAAGT TAAATACTGG GAGTGTCTTA   540
AGCTCTAGTA TGACTTTATC GGAGCTTTAT AATGAATGGC TGGATTTAAA AATTTTACCT   600
AGCAATAGAA GTGTAGTTAC TAAAAAATAA TATCTTATGA GAAAGAAGGT CATCGAAAGG   660
TTATTTGGAA ATAAGCCTGT ATCACAAATT AAGCCTAGCG AGTATCAAAA AATTATGAAT   720
GAGTATGGAG AGACTGTATC GAGAAATTTT TTAGGAAGAT TGAATTCTAG TATCCAGGCA   780
AGTATACAGA TGGCTATTGC TGATAAGGTG ATAATAGAGG ATTTTACTGC TTATGTTGAG   840
TTGTTCTCTT CTAAGAGTGG ACACAAAGGT TGAGGAAAAG TATCTACATA CTGAGTCAGA   900
TTATCAAAAA GTTTTAGTAT ATTTGAAAAA TAAGTTTGAT TATCAGAAAT CTATTGTACC   960
GTATGTAATT TATTCCTTT TAAAACTGG CATGCGTTTC TCCGAATTGA TTGCTCTAAC  1020
TTGGGATGAA GTTGACGAG                                     1039

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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

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CTGAGAAGTC AGGAAGGCGA TGTGGAGAGA TTGAGGAATT GGATACTTAA CTCCATAGTA    60
ATCTTCGTAA AACTCGATAG AGCGAACAGC GATATCCAGT GAGAAATCAA GATTTGAAAG   120
TGGATGTGCT TTGGTTGAGT AGACACCCTA CCAGGGTACC ATTTTGTAGT TTAGCGGTCA   180
CCCCTTGCAA ATCACCAGCA ACAAAGGCCA ACAAGTAAGA AGACATGCGA GGTGTTGTCT   240
CAAACCTCCA GATACCTGTT TCCTTACGGT TTTCAACATC GATTCTGGC ATGTTTGACA   300
AGGCCAATTC ACCTTCTGCT TGGTCAAAGC GAAGAGAGAG GTCAAAAGTT GCTTTGGCTT   360
CAGGCTCATC CACACATGGG AAAGCTTCGC GCGCAAAATG GCTCTCGAAC TGAGTAGACA   420
AGACCTCCTT CTTGACTCCA TCAACTGTAT AATAAGAAGG GTAAATCCCT GTCATGTTGT   480

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CTGTAATTTT	ACCAGAAAAG	GCAAGAACCA	ATTCAACTTG	ACCAGCCTCA	GCCAATTTCGA	540
TATGAAGGGC	TTCATTGTCA	TGGTCAACTG	TAAATGGACG	AGCTTGACCT	GCAACTTCTA	600
CAGAGGTGAT	TTCCAAGTCT	TTTTGGTGGA	GGGAGATGCG	GTCACCTCTGT	GCTTGACCAG	660
TGATGGTCAC	TTTCCCAGAA	AAAGTCTTGG	TCTCACGACT	CAAATCTAAA	AATAAATCAT	720
AATGTTTCAGG	AACAAATTGC	TTAATAAAAT	GTTCAACTGC	TTGCATAGTT	TTCTCCTATT	780
CTAAGTTTAA	GAG					793

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGATGATTT	GCTTTTCATC	TATGATAAAG	TCTTTGTTGA	GCGTCGGAAT	CTCTACTGAC	60
TGGAAATTTT	CCGTAGATAA	TCCAAATGCC	CTTTAAAGAA	AACCTCATCT	GTCAACACCG	120
AAATCATCAC	TGCTCCGTTT	TCTTCATAAG	TCTGGGCCTG	TTGCACAATA	TCCACATCGA	180
GATTGATATC	TCCCCAAAAC	TAGGGCTAGC	TTTCTTGACT	TCAGCGATTA	CCTGCAAGCG	240
GTCTGATGA	TTCTTCAAAA	ATTCTGCCAA	GCGATAGGTC	TGGCGCAGAG	GCTGGATTTG	300
CTCCAGCTTC	ATCTGCTCCA	CCTCACGCGC	CTTCTGCTCT	AAGATTCTGT	CTAAAAATTC	360
CTGACTCATT	TTTGGTACTC	CTGTAACAGT	CTGAGTTTTT	CAAGGGCCTT	GCCTCTAGCA	420
ATCACTTGAC	GGGCCAAGGC	AACTCCTTCC	TTGATGCTAT	CAATCTTACC	ATTAGCATAG	480
AAACCAAGAC	CAGCATTCOA	GACTGTCGTT	TCCAAGAATG	GACTTGCTTC	GTTTTTCAGA	540
ACGCTAAGCA	AAATTTCTGC	ATTTTCCTGA	GCATTCACAC	CACGAATATC	TTCCATAGCA	600
TAGCCTTCCA	TTCCCAAATC	CTCTGGAGTA	AAGCTTGACA	AG		642

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTCTTGCAGG	TTATTAAGGA	GAAAACGGAG	GTAATAGAAG	TATGATTTAT	ACAGTCACAC	60
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TCAATCCATC CATTGACTAT ATCGTTCGTT TGGACCAAGT CAAAGTTGGT AGTGTAATC	120
GTATGGACAG TGATGATAAG TTTGCTGGTG GGAAAGGAAT CAATGTCAGC CGTGTCTTGA	180
AACGTTTGAA TATATCAAAT ACAGCGACGG GATTTATCGG TGGCTTTACT GGTAAATTTA	240
NCNCAGATAC TTTAGCAGAG GAAGAAATCG AGACNCGTTT TGTCCAGGTG GCAGAAGATA	300
CTCGTATCAA TGTTAAAATC NAAGCAGACC AAGAAACAGA AATCAACGGA ACGGGTCCAA	360
CTGTTGAACC GGTTAAGCTA GAAGAATTGA AAGCTATTTT ATCTAGTCTG ACAGCAGAAG	420
ATACAGTTGT CTTTGCAGGT TCAAGTGCTA AAAATCTAGG CAATGTTATC TATAAGGGAT	480
TTAATCTCCT TGACGCGCCA GACTGGTGCG CAAGTGGTCT GTGACTTTGA AGGACAGACC	540
TTAATTGATA GTTTGGATTA CCACCCTCTT CTTGTAAAC CAAATAATCA TGAAC TTGGA	600
GCGATTTTGG GGGTTAAACT CGAAAGTTTA GATGAAATTG AGAAATACGC TCGTGAGTTA	660
CTGGCTAAGG GTGCTCAAAA TGTATTATC TCTATGGCTG GTGATGGTGC CCTTCTTGTC	720
ACATCTGAGG GAG	733

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAAGGGAAG TAGGAAAAGT ATGTATCCAG ATGATAGTTT GACATTGCAA CACGGACTTG	60
TACCAGATCA ACATGATGCA GGT TACTTT GATCAAGGGA TTTACAATAA GAAGGCGGTC	120
TTTGAGGTGT ATTCCGCCA ACAGCCTTTT AAGAACGGCT ATGCGGTTTT TGCAGGTTTG	180
GAAAGAATTG TGAAGTATCT TGAAGACTTG CGTTTTTCAG ATAGTGATAT AGCCTATTTG	240
GAGTCGCTTG GTTATCATGG GGC GTTCTTG GATTACCTTC GCAATTTCAA GTTGGAGTTG	300
ACCGTTCGTT CTGCCCCAGA AGGGGATTTG GTTTTTGCTA ATGAACCGAT TGTGCAGGTG	360
GAAGGACCTC TAGCCCAATG TCAGTTGGTC GAAACGGCTC TTTGAACAT CGTCAACTAC	420
CAGACCTTGG TGGCGACGAA GGCAGCCCCC TATCCGTTTG GTTATCGAAA ATGAACCCCT	480
GATGGAGTTT GGGACACGTC GGGCTCAAGA AATGGATGCG GCCATCTGGG AACACG	536

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCCCCTGT	AAGGCTGGAC	GATTGCCTTT	CTTAGTATCC	GCAAAGAGGT	AAACTGAGAA	60
TAGAGAGGAT	TTCTCCTTCA	ATATCTTTGA	CAGACAGGTT	CATCTTGCCT	TCTACGTCTG	120
AAAAAATCCG	CATATTGACC	AGTTTTCTCA	CAGCATAGTC	CAAATCTTCC	TCTTGGTCCT	180
CTGGTCCAAC	ACCAACCAGC	AATAAAAGTC	CCTGATTGAT	TTTTCCCTGA	ATCTGGCCTT	240
CTATACTCAC	TTGGGCTTTT	TTAACCCGTT	GGATAATGAT	TTTCATAATA	GCCTTTCTAG	300
TAAGAGCTAG	GACAAC TAGC	CGTTGGTCCG	TTGACAGAG	TAAACTTCTG	GCACACTCTT	360
AATTTTATCG	ACAACCGTGG	TCAGTGTAGA	GAGGTTGGCA	ATACCGAAGG	ACACATGGAT	420
ATTAGCAAAC	TTCATATCCT	TGGTTGGTTG	GGCATTGACC	GTTGAAATAT	TCTTGGTTGT	480
ATTTGAAAGA	ACTTGCAGTA	CATCGTTCAA	CAGTCTGTGA	CGGTTGAGAC	CGTAGATATC	540
GATATGGGCC	ATATACTCCT	TATTTGAG				568

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTTTATATTG	TACCAAGTAT	CATTTCTAGT	GCTGCTATGG	GCTTGATTTT	TCTTCAAATC	60
TATAATCCAA	ACTATGGTGT	TGTTAACCAA	ATTATTCATC	TATTTAATCC	ATCGTTTAAA	120
GATTCAGTAC	TGTTGACTCC	CAGGATTAAA	AATAGTAGCT	ATGACTGGCG	CTTATATCTT	180
CTTTGCAGGA	GCATCAACCA	TTATGATTTT	TTGGGCAAAT	TTTGTCTATT	CCAGAAGAAG	240
TTCAAGAAGC	TGCTATTTTA	GACAATATTA	CTGGTTGGAG	GAAAGAGTGG	TATATTACGA	300
TTCCGATGAT	TAAGGGGACA	ATTAAAACTG	TTTCAATTAT	GGCAGCAACT	TCAGGATTTT	360
TGCTCTATAA	CGAAGTATTC	TTTTTGACAA	ATGGTGCTGC	AGGAACAAAA	AGTATCAGTT	420
TTGTTATTTC	AGAATTAGCA	GTGGCTAGCT	CACGAACTCA	GTATGCTCGT	GCAAAATACAA	480
TTGGAGTTAT	ACAAATCTTA	GGTGGGAATG	TGATTATCGT	TTGTATTAAT	ATTTTATTCA	540
GAGAAAGAAA	AAGACTGAAA	GGTGGGAAAT	GATTATGAAT	ACACATATAA	ATGGTATTAG	600
TAAAAAAGGC	AAAGTTCTTA	TATATGGTTA	TATGCTCCTT	ACCATTTTAA	TTTCTATTTT	660
CCCTATTGCG	TGGATTTTTT	TATCATCATT	AAAAGCAGAT	CCTATGAAAA	ATCCAGGTAT	720
TAGTTTACCG	ACTGACTTTA	CTCTGAAGG	TTATATAAAT	GTTTTTACAA	AACTTCATGT	780
TTTTACTTAC	TTTTGGAATA					800

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

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CTCAGTATTA TCCCTACCAA AATGAACGTC AGTTAGTGAC TCAGGTGGTT TGGGAACAAT    60
GGGCTTTGGA ATTCCAGCAG CAATCGGTGC TAAAATTGCT AACCCAGATA AGGAAGTAGT    120
CTTGTTTGTT GGGGATGGTG GTTTCCAAAT GACCAACCAG GAGTTGGCTA TTTTGAATAT    180
TTACAAGGTG CCAATCAAGG TGGTTATGCT GAACAATCAT TCACTTGGAA TGGTTCGCCA    240
GTGGCAGGAA TCCTTCTATG AAGGCAGAAC ATCAGAGTCG GTCTTTGATA CCCTTCCTGA    300
TTTCCAATTG ATGGCGCAGG CTTATGGTAT TAAAACTAT AAGTTTGACA ATCTTGAGAC    360
CTTGGCTCAA GACCTTGAAG CTACTACTGA GGATGTCCT ATGCTAATTG AGGTAGATAT    420
TTCTCGTAAG GAACAGGTGT TACCAATGGT ACCGGCTGGT AAGAGTAATC ATGAGATGTT    480
GGGGGTGAAG TTCCATGCGT AGAATGTTAA CAGCAAACT ACAAATCGT TCAGGAGTAC    540
TCAATCGCTT TACAGGTGTC CTATCTCGTC GTCAGGTTAA TATTGAAAGC ATCTCTGTTG    600
GAGCAACAGA AGATCCGAAT GTATCGCGTA TCACTATTAT CATTGATGTT GCTTCTCATG    660
ATGAAGTGGG GCAAATCATC AAACAG                                     686

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(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

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TTTTCCCAGC TATTTTACTG AGTATAAAAG CCTTATTTAA CTTACTCTAT GTACTCGGTT    60
TTCTAGGAGG AATGTTGGGA GTTGGGATTG CTTTGGGGTA CGGAGTGGCC TTATTTGACA    120
AGGTTCGGGT GCCTCAAACA GAAGAATTGG TGAATCAGGT CAAGGACATC TCTTCTATTT    180
CACAGATTAC CTATTCGGAC GGGACGGTGA TTGCTTCCAT AGAGAGTGAT TTGTTGCGCA    240
CTTCTATCTC ATCTGAGCAA ATTTCCGAAA ATCTGAAGAA GGCTATCATT GCGACAGAAG    300
ATGAACACTT TAAAGAACAT AAGGGTGTA TACCCAAGGC GGTGATTCGT GCGACCTTGG    360
GGAAATTTGT AGGTTTGGGT TCCTCTAGTG GGGGTTCAAC CTTGACCCAG CAACTAATTA    420
AACAGCAGGT GGTTGGGGAT GCGCCGACCT TGGCTCGTAA GGCGGCAGAA ATTGTGGATG    480
CTCTTGCCCTT GGAACGCGCC ATGAATAAAG ATGAGATTTT AACGACCTAT CTCAATGTGG    540
CTCCCTTTGG ATCGAAATAA TAAGGGACAG AATATTGCAG GGGCTCGGCA AGCAGCTGAG    600

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GGAATTTTCG GTGTAGATGC CAGTCAGTTG ACTGTTCCCTC AAGCAGCATT TTTAGCAGGA	660
CTTCCACAGA GTCCCATAC TTA CTCTCCT TATGAAAATA CTGGGGAATT GAAGAATTGA	720
TGAAGACCTA GAAATTGGCT TAAGACGGGC TAAGGCATTC TTTACAGTAT GTATCCTACA	780
GGTGCATTAA GCAAAGACAA TT	802

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACTATTTT AGCATAAAAA TGCCCAAAGG GGGNGCCGTG TGTTTACTGA TTTTCAGGNT	60
AATGGACCAG GNAAATCAGC ATGAAAATAA AAAGAGAAAC AGATTATTTT AGCCATTTGT	120
CAGATTTATG CTATGCTTAA GGTAGAAAAT GAAAGGGATA ACAAATGTAT TTAGGAGATT	180
TGATGGAGAA AGCCGAGTGT GGTCAATTTT CAATCCTTTC CTTTCTATTA CAAGAGTCTC	240
AGACGACCGT CAAGGCTGTA ATGGAAGAAA CAGGATTTTC AAAAGCAACC CTAACCAAAT	300
ATGTCACCCT GCTCAATGAC AAGGCTTTGG ATAGTGGCTT AGAACTGACT ATTCACTCAG	360
AAGATGAAAA TCTGCGTCTG TCTATAGGTG CAGCTACTAA GGGGAGAGAT ATTCCGGAGC	420
TTGTTTTTTG GATAGTGCTG TTAAATACCA GATTTTGGTT TATCTTCTCT ACCACCAACA	480
GTTTTTAGCC CATCAGCTGG CTCAAGAATT GGTGATTAGC GAGGCTACGC TTGGTCGTCA	540
CTTAG	545

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAGGTCAAGA TTGATTCCCA AGGTTNGAGG AATCTGCGGA ACCAGATTTA GAAGAAATCG	60
AGCGGTTACC ATGCTTGGCC ATGTGAATAC CGCCACCAGC CAAGACAAAG GCTGCAGTTG	120
TGGAAATATT AAAACTGAAA GACTTGTCCT CACCTGTACC ACAGTTGTCC ATAGCATCAT	180
GAATCTCAGT TGGAAATATG TGGGCATGTC CTCTCATGAC TTGGGCAATG GCTGTGCGTT	240

CTTCAGGTGT TTCCCCCTTC ATCTTAAGAG CTAAGAGGAG AGAAGCAATC TGCCTTCAG	300
TTACACGCCC AGTTACGATA CGCTCAATGA CATCCGTCAT TTCCACACCT GATAAATTTT	360
CAAATTTTGC TAGTTTTTCA ATAATCTCTT TCATCCTAGT TTCCTCACTT TACAACCTCC	420
TCGATAAAAT TCCGAATAGA AGACAAGCCG TCTGGCGTTC CAATGCTCTC TGGATGGTAC	480
TGGAAGCCAT AAATCGGTAG GTTTTATGT TGAATCCCCA TGATGGCTTG GTCATCAGTC	540
GAACGAGATC AAGCTTATCG ATACCGTNGA CCTCGA	576

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTAAAGGGA GGCGAACATG GCCCAAGATA TAAAAAATGG AGAAGTAGAA GAAGTTCAAG	60
AAGAGGAAGT TGTGGAACA GCTGAAGAAA CAACTCCTGA AAAGTCTGAG TTGGACTTGG	120
CAAATGAACG TGCAGATGAG TTCGAAAACA AATATCTTTC GCGCTCATGC AGAAATGCAA	180
AATATCCAAC GCCGTGCCAA TGAAGAACGT CAAAACCTGC AACGTTATCG TAGCCAGGAC	240
TTGGCAAAAG CAATCTTACC ATCTCTTGAC AACCTTGAGC GTGCACTTGC AGTTGAAGGT	300
TTGACAGATG ATGTGAAGAA GGGCTTGGGG ATGGTGCAAG AAAGCTTGAT TCACGCTTTG	360
AAAGAAGAAG GAATTGAAGA AATCGCAGCA GATGGCGAAT TTGACCATAA CTACCATATG	420
GCCATCCAAA CTCTCCCAGC AGACGATGAC CACCCAGTAG ATACCATCGC CCAAGTCTTT	480
CAAAAAGGCT ACAAACCTCA TGACCGCATC CTACGCCAG CAATGGTAGT GGTGTATAAC	540
TAAGATACAA AGCCCGTAAA AAGCTCGCAG TAAAAATAGG AGATTGACGA AGTGTTCGAT	600
GAACACAAGA AAATCTANCT TTTTACTCA GAGCTTAGGG CGTGTTCGAT TCGGCAATTC	660
TGACGGTAG	669

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTAGTTCACC	ATTTCTATTT	AAATTCGGCT	CAACTACACC	GAAATATCAT	ATAAGGTAAA	60
GTTCCCACTA	AGAATCTCAG	AATGAAATTC	TTCACAACT	TCAGCGGTCA	AACCTTAGCTT	120
ATCCAATTTT	AGACCGATAA	ACCCATACTT	CAGAGATACT	TCCTCTTGAA	ATTTAGAGTA	180
ACTCTTATTA	GACATTTGAT	GTATCGTTAT	CGGGCTATTA	GAAGGAGCCC	GATTTAAAC	240
TTCTTTATTC	ATGAAATTTT	TCCTTCAAAA	AACAAAACAT	TCTATATACT	TAAATTTTAG	300
GGCAAGACTG	CCGTTCCACT	GACCACGCTC	CACCTGCCAG	CAAAGCTGGC	AGGTCCAGCC	360
TTACCCTAAA	TATAAATTAT	TTAATTTTGT	CCATTTCAT	CAATTCTGCA	AAGGTCCCAA	420
GCTTTCTGGA	TTGAATTACC	TCATATTGGG	CATTCTGTCC	AAATGAAGCA	TTATTAATCA	480
CTTCAACCTC	ATAAAGGCCT	GGAGCAGAGA	AAACAGCTCC	AAATTTGGAT	TTATCGAAAT	540
GCATACCTAG	GTCACCTCAA	CAATCATTA	GGGTGGAGAC	TTTTATCCAG	CCTCGTTCTT	600
TCTTAGTAGA	AATAG					615

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTACTGTAGT	TGGAAGTGT	GAAAAACAAG	GAAAAACAAA	GAAAGTTGTT	ACTTACAAGT	60
ACAAACCTAA	AAAAGGTAGC	CACCGTAAAC	AAGGTCACCG	TCAACCATAT	ACAAAAGTTG	120
TCATCAACGC	AATTAACGCT	TAATTTTAAG	GAGAACACAT	GATACAAGCA	GTCTTTGAGA	180
GAGCCGAAGA	TGGCGAGCTG	AGGAGTGCGG	AAATTACTGG	ACACGCCGAG	AGTGGCGAAT	240
ACGCTTAGA	TGTCGTGTGT	GCATCGGTTT	CTACGCTTGC	CATTAACCTT	ATCAATTCTA	300
TTGAGAAATT	TGCAGGCTAT	GAACCAATCC	TAGAATTAAA	CGAAGATGAA	GGTGGCTATC	360
TGATGGTTGA	AATACCAAAA	GATCTTCCTT	CACACCAGAG	AGAAATGACC	CAGTTATTCT	420
TTGAATCATT	TTTCTTAGGT	ATGGCAAAC	TATCGGAGAA	CTCTTCTGAG	TTCGTCCAAA	480
CCAGAGTTAT	CACAGAAAAC	TAACACGGAG	GAAAACATTA	TGTTAAAAAT	GACTCTTAAC	540
AACCTGCAAC	TTTTTCGCCA	CAAAAAAGGT	GGAGGTTCTA	CATCAAACGG	ACGTGATTCA	600
CAAGCGAAAC	GTCTTGAGC	TAAAGCAGCT	GACGGACAAA	CTGTAACAGG	TGGATCAATC	660
CTTTACCGTC	AACGTGGTAC	ACACATCTAT	CCAGGTGTAA	ACGTTGGTCG	TGGTGGAGAC	720
GATACCTTGT	TCGCTAAAGT	TGAAGGCGTA	GTACGCTTTG	AACGTAAAGG	ACG	773

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGGATAATT	GGAGCAATTC	CTGATGCCAG	TTTGAGGTTA	CTGATAGGAT	TGTGGGCGAT	60
AGCCACTTGA	GAAGATGCCA	AGAGTTCAAT	TTCTCTCTCG	TTTAATTCTGA	CCCCGTGAGC	120
AAATACGGAC	GGATGATCTA	AATAACCCAG	TTCTTCAAGA	AAAGCAAGGG	GGCGTTTGCC	180
GTACCGTTTG	AGGATAATTC	CTGACTCCTC	CTTGGTCTCC	GCCACATGGA	CATGGAGCGG	240
AATATTTAGC	TCTTTTGCCA	TTTCCAAACT	CGCTTCCAGC	AAGTCTCTAC	TGCAGCTATA	300
CGGAGAATGA	GGTGCTACCA	TAACCCTTGA	AATTTGGGAT	TTTTATATTT	TAAGATTTCCG	360
TCTATGATGG	ATCGAGTTCT	GCTTATAGTC	TCAGCAGTTG	TTTCTGTCTC	TGAAGAAAAG	420
AGAGTCGGAG	AAAAATAACA	ACGCATCTTG	GAAGTTTCA	CCACCTGATA	AATTTGCTGG	480
ATATCCACAC	CATTGGGATT	ATACATATCG	TTAAAGGTTG	TTGTTCTCTGA	CTGGAGCATC	540
TCTGTTAGGG	CTTCTTTGAC	CGCATTGGTA	GTCATGTCGG	GAGTAAACTC	AGATTCTGCT	600
GGCCAGATAT	AGTCATTGAG	CCATTTTCATG	GAGATTGCTG	TCATCTCGGA	TCCCTCTCAG	660
ACCTGTCATT	GCAGAAATGGG	TGTGACAATT	GACCAAACCA	GGCATAAGCC	AAG	713

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTAGAAAATC	TGCTTTTTTC	TCGAAAAGTT	TAATACTTGG	TACAATATTA	CGCTTGCTTT	60
GCTCGGCTGC	TCCAAGGGCA	ATTTTTTCTA	GTTTTTCAAC	TTTTTTACCC	AATTTCTTGC	120
CATCCCACCT	GGCAACTGAC	CAGTCTGCAG	GAAAGGCCCA	GATTTGGCTA	GCACCCAGTT	180
CGGTTACTTT	TTGAGCGATG	AACTCCAGCT	TGTCTCCCTT	GGGAAATCCA	GATGCGATGG	240
TCACTTGGAC	TGGTAGTTCC	ACATTGTCAT	TTAATTCTTG	GACCAACTCA	AACTGACGAT	300
TTTCCATATC	CAGCACGCGC	GCCAAGCGCT	TGATGCCATC	ATCAAAGACT	AAGGTAACCT	360
CATCCTCTTC	TTTCAAGCGC	ATAACCTGAA	ACATATGCTT	ACTGGTTTCC	TTGTCCTCGA	420
TAGTGACAGG	AGAGATAGCA	CTGCCTTTTA	CAAAATACTG	CTGCATGCTA	GCCTCCAATC	480
ACACCAGAGA	TATCCTTGGT	TTTCTTAAAG	ACACAGGTAT	TCCATTCCCC	TTGAACCATG	540
TGAGTTTCGA	GGAAAAATCC	AGCTGATTCA	GCCGACTCGC	GCACCATGTC	CCACTTATGC	600
CTTGAATAAT	GCCACTCATG	ATCAGGTAGC	CTTCGTCTTT	AACCAAACGA	TAGGCATCGT	660
CTATTAGATG	AATGAGGATA	TCCGCCAAGA	TATTAGCCAC	AATCACATCT	GCCTCAATTT	720
CCACACCCTT	AAGCAAATCT	CCAGCCGCTA	CATGGATATT	TTCCATGCCA	GGGTTGAG	778

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

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CTTCCCAGAT TTTTCGTTG ACTTGCTGTT CAATCGCACG CAATTCTTCA GCAGTTACAG      60
CTTGGAAGTG GGTAAAGTCA AAGCGAAGGA ATTCAACTTC GTTAAGAGAT CCTGCCTGTG     120
TTGCGTGGTT TCCAAGGATA TTGTGAAGGG CAGCGTGAAG CAAATGAGTC GCAGTGTGGT     180
TTTTCATGAC ACGGTGACGG CGATTGCTAT CAATTGCCAA GGTATATTCT TGGTTCAAGG     240
CAAGCGGTGC AAGGACTTCA ACTGTATGAA GGGCTTGACC ATTTGGGGCT TTCTGAACAT     300
TGGTCACAGT AGCCACAACC TTACCTGACT CATCCAAGAT TTGTCCGTAG TCAGCTACCT     360
GTCCACCCAT TTCAGCATAA AATGACGTTT CCCGCAAAGA TAAGAGAGGC AGTTCCTTCT     420
GAAACAGCTT CTACTTCTGC ATTGTCCGCC ACGAATAGCT ACCAATTTAG AAGACAATTG     480
GCTAGCATTG TAGTTGAAGG CACTTTCTAC AGTGATGTTT TGAAGAGTTT CCATTTTGCA     540
TACCCATTGA GCCACCCTTG ACAGCTGACG CACGCGCGCG TTCTTGTTGT TCTTTCATGG     600
CTGCTTCAAA ACCTTCACGG TCTACAGTCA TACCAGCTTC TTCAGCGATT TCTTCAGTCA     660
ATTCAACTGG GAACCCATAA GTATCATAGA GTTTGAAGAC ATCTGAACCA GCGATAACAG     720
ATTGACCTTT TTCTTTCAAG TCTGCTACAA TGCCTTGGGC AAAGTGTTGA CCTTGAGTGA     780
AGGGTACGGG CAAATGATTC TTCTTCGCCT CTTAACGATT TTCTCAATAA AGTCACGTTT     840
CTCAAGCACT TCTGGGTAGT AGCTTTCCAT GATTTTCCA ACAGTTGGAA CGAGTTTGTG     900
AAAGGAAAGG CTCGTTGATA CCCAATTTT GACCCATGCA TAGAAGCACG ACGGAGAAGA     960
CGACGAAAGG ACATAACCAC GACCCTCCAT TTCCTGGAAG GGCACCATCC ACCGATGGCA    1020
AATGAAAGTG AACGGATGTT GGTCCGCGAA TGAACCTTGA AT                                1062

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(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTCAAAGGTC GCACCTGCAA TACGACCCGC TACAGGACCT ACACTTGCTC CATGCTTGGG	60
ACTATTGCCT ACATAACTAC CAAAGTCATC AAATCCCAAG ATAACATTGG CAAAATTTCC	120
AGCCTTGTC GGTGCGACAT AGCGCAAGAT AGTCGCACCA TAAGTCATAA CCTCAAGTTG	180
GTAGCCACCG TCTGTCTCAA ATCGATAGGC CAAGACATCC TCACCCTCAA CATTTCCAAA	240
TACACGCTCT GTGTATGCTT TCATTCTGTT CTCCTTTTAC TATTTCTCTC AAGCAAACAA	300
ACCATAGAAA GCGTACTGAC AATCTATGGT TTATCTGATA ATTTACAAAT CCTCTTGTC	360
AGAATTCATA AACACTGTCT TACTTTTGAT ATTCGTGAAT TATGACACCT TGTACTACAC	420
GGTTTACTGT ACCTGTAGGA GACGGTGTAT CTGGTTTATT TTCTACCTTG AGTGAAGTCA	480
ATAGGGCAAA GAGTTGGGCA TAAACGATGT AAGGGAAGAC ACGGTAAATA TCATTCAAGA	540
CACCGCCACA ACCAAGGGCC ACTTCTTTGA CATTTTCAAG ACCAAAAGCT TGATCACTCA	600
AAAGCACAA CACGACGAGCA ATCTGGTCAC CAGCAACTTC ACGAACCAAG TCCAAGTCGT	660
ACTTACGAGT GTAGTCCGTC CTTGTACCAA AGAACAAAAC AACTGTATTG TCGTTGATAA	720
GATATTTGGA CCGTGACGGA ACCAACTGGG CTTTCATACA TGGTCGCAAC TTGAACAACA	780
GTTAATCCCA AATCTTGAGC TGAGCCTCAT GAGCAGTCCA AAGAAGACCA GCGCCTAGAA	840
GAGACCGGTT AAGTCTTAAT CACAG	865

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTGCTCCA GTTGATAAGA AAGGCTTGGT CGATGTTGAG GCGTTAGCAG GTTTGATACG	60
GCCTGATACA ATCCTCGTTT CCCATCATGG CTGTGAACAA TGAAATCGGC TCTATCCAAC	120
CNATTGAGGC TATTTAGAAA TTCTTGCGAG ACAAGCCGAC TATTTCTTTC CACGTTGATG	180
CGGTTGAGGC GCTTGCCAAA ATTCCGACTG AAAAGTATCT GACAGAACGG GTGGATTGCG	240
CGACCTTCTC GAGTCATAAA TTTCATGGTG TCCGTGGTGT TGGCTTTGTC TATATCAAAT	300
CTGGCAAGAA GATTACACCT CTTCTTACAG GTGGTGGCCA GGAGCGAGAT TATCGTTCTGA	360
CAACTGAAAA TGTGGCAGGG ATTGCAGCGA CAGCCAAGGC TCTCCGTTTA TCTATGAAAA	420
AGCTAGATAT CTTTAGGAGC AAGACTGGGC AGATGAAGGC AGTGATTAC CAAGCTCTTC	480
TGAATATCC GGATATTTTT GTCTTTTCAG ATGAGGAAGA CTTTGCACCT CATATTCTGA	540
CTTTTGGAAT CAAAGGTGTT CGAGGTGAAG TCATCGTTCA CGCCTTTGAA GACTATGATA	600
TTTTCATCTC AACAACTCA GCTTGTTTAT CTAAGGCAGG AAAACCAGCC GGTACCTTGA	660
TTGCCATGGG AGTGGACAAA GATAAGGCCA AGTCAGCTGT GCGTCTTAGC CTAGACTTGG	720
AAAATGATAT GAGTCAGGC GAGCAGTTTT TGACCAAGTT AAAATTGATT TACAATCAAA	780
CTAGAAAAGT AAGATAGGAG CATTATGCA GTATTAGAA ATTATGATT GCTACGGAGA	840
GTTGTCAACC AAGGGTTAAA AACCGTATGC GTTTTCATCA TAACTTCGT AATAATATTT	900
CGGACGTTTT GTCTATCTAT ACCCAAGTTA AGGTAACAGC AGATCG	946

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTTGCTCGTA ACAGGTGCTA TCCTTGGTGT CAATGTTTAC ATCTTCTCAC CAAAAGAACT	60
CTTCCCAGAA AAAGAAATCG TTGAATTGGC AGAAGGATTT GCTAAAGAAA GTGGCGCACA	120
TGTTCTCATC ACTGAAGATG CTGATGAAGC AGTTAAAGAT GCAGACGTTT TTTACACAGA	180
CGTTTGGGTA TCAATGGGTG AAGAAGACAA ATTTCGAGAA CGTGTAGCTC TTCTTAAACC	240
TTACCAAGTC AATATGGACT TAGTTAAAAA AGCAGGCAAT GAAAACCTGA TCTTCCTACA	300
CTGCTTGCCA GCATTCCACG ATACTCACAC TGTTTATGGT AAAGACGTTG CTGAAAAATT	360
TGGTGTAGAA GAAATGGAAG TAACAGACGA AGTCTTCCGC AGCAAGTACG CTCGCCACTT	420
CGATCAAGCA GAAAACCGTA TGCACACTAT CAAAGCTGTT ATGGCTGCTA CACTTGGTAA	480
CCTTTATATT CCTAAAGTAT AATTTTAGAT AATAAACCGT CTACCAACAG CTATGAGGGC	540
TGCGACTAAT AG	552

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTAAAAAAG TCAAGTAGAA AACGAATATT CTAATTAACT TGCACGAAAT TATTTTTCAC	60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTTC	120
CTGGTAGACC ATTTGGCTCA GTCACCTCAT AGCCTTTTGT ACTGTGCTCT TGATGAAGTG	180
CCTCAAGATC AGGTGTACTG AGGGCGATAT GGGCAAACCC ATCACCACCC ACATACGGAC	240
CGTGATCGTA GTTATAAGTC AACTCCAACCT CATAGTCATC ACCCTCAAGA CCTAGATAGA	300
CAATCGTGAA GGCATGGTCT GGAAATCTC TGCGACGCAA TTCTTTAAAA CCAAAGCAT	360
CTTGATAAAA TGCAATTGAT TTTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATTT	420
TTGAAGCCAT ATCTTCTCTC TTTATTTTAA AAAAGACTGG ACAATCCTGT TCCAGTCTCA	480

TCAGTTGTTA TTTACCAAGT TTTGCTTTAG CT

512

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

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CTGGACCACA CTATTTTCTG TGTGGCTAT CGTGTCATGC AAAAGGATCT AGAAGGGACG      60
CTGGATGCTG AAAAAGTCAA GGCTGCTGGT GTTCCGTTTCG GCCCGCTTTT TGGTAAAATC      120
AAAAACGGCC AGGATCTTGT TTTGGAAGAC GGAAGTGAAG TCAAGGCAGC AGACTATATC      180
TCAGCGCCAC GTCCAGGTAA GATTATCACT ATTTTAGGAG ACACTCGAAA AACGGATGCC      240
AGTGTGCGTC TGGCTGTCAA TGCAGATGTC CTAGTTCATG AGTCCACTTA TGGCAAGGGT      300
GATGAAAAAA TTGCTCGTAA CCATGGTCAC TCAACTAATA TGCAAGCTGC ACAAGTAGCG      360
GTAGAAGCAG GTGCCAAACG CCTCCTACTC AACCATATCA GTGCCCCGTTT CCTCTCAAAA      420
GATATAAGCA AACTCAAGAA GGACGCTGCC ACAATTTTGT AAAATGTCCA TGTGGTCAAA      480
GACTTGGAAA AAATGGAAAT CTACCAGTCA CAGAAAGGAT AAGTATGCCT ACTATTCTCC      540
ATTAACCGGA A

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551

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

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CCGTCATTAT ACCTTTGTCT ATGAAAATGA AGACCTAGTC TATGAGGAGG AAGTCTTATG      60
ATACAGCCAG CAAGTTTAGA AGAATTAGCA TCTTTAGTGG AAAAAGCGGG CAAGAAGGTC      120
TTCCTTTTGT TGGCAGACTG GTGTGGCGAT TGTCGTTATA TTTATCCTGC CTTACCAGAG      180
ATTGAGGAGA CCAATCCAGA GTTCACCTTT ATTCCAATGG ACCGAGATCA GTATATGGAT      240
TTGGCCAAAC TCTGGGATGT TTACGGAATT CCTAGCCTTG TTGTTCTAGA AAAGGACAAG      300
GAAATTGGTC GTTTTGTCAA TCGCGACCGT AAAAGTAAGG AGCAAATTAA CGATTTTTTA      360
GCAGGATTGA AATAGGAGAA AAAGGAAACA ATGATTTTTA CGTATAACAA AGAACATGTC      420

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GGTGATGTCC TTATGGTCAT CGTGAAAAAT AGCGGAGATG CCAAAGTCAA TGTGGAACGC	480
AAAGGCAAGG TAGCCCGTGT TTCCTCAAA GAAATGGGG AAACAGTAG	529

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTAGGATAGA CCGCTTTTTA GCATTTATCT AAGCATTCCA GAGTACATGT ATCTTGCATG	60
TGCTCTTTCT TTTGGGGTTG AAACGATAGG AGAAGGAAAT GTTAGAATTG CTAAATCAA	120
TCGATGCTTT TGCTTGGGGA CCGCCCTCT TGATTATTG GTCGGAACAG GGATTACCT	180
AACCATGCGG CTAGGACTCT TGCAGGTTTT GCGTCTGCCC AAGGCCTTTC AGCTTATTTT	240
TATCCAGGAT AAGGGACATG GTGATGTATC CAGTTTACA GCTTCTGTG TAACAGGCCC	300
TTGGGCATTC AAAGTGGTTG GGAAACAGGG AAATATCCAT TAGGGAGTTG GCGACGGCTA	360
TCAAGGTTGG TGGACCAGGA GCTCTATTTT GGATGTGGAT GGCGGCTTTC TTTGGAATGG	420
CTACCAAGTA TCGGAAGGA CTCTTGCCCA TCAAATACCG CACCAAGGAC GACCATGGTG	480
CAGTAGCGGG AGGTCCCATG CATTATATCC TTCTAGGGAT GGGAGAAAAG TGGCGACCAC	540
TTGCTGTTTT GTTGCAGTA GCAGGAGTAT TGGTGTCTCT CTTGGGAATC GGAACCTTCA	600
CCCAAGTCAA CTCGATTACA GAATCTATCC AAAATACAAC GACGATTTCG CCAGCCATCA	660
CAG	663

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTTGACCAC CAATTCTTCA CCCGATATGA TGCGCCCTGC TCGCTGAGCA AGCCCCAAGA	60
GATTACTTAT CTTTGCTTA TTCAAGTCCC AACTCTCTTC TTTTCACTTT GTGATCCACA	120
TAAGCGATCA ACTCGTCATA AAAGCTTTCT TCCACTTCCA TGCTAAAGCT GCGGTAAAG	180
ACCTTCTTCT TTTTCGCTC TAGGGCTTCT GCATTGTCTA GTTTGATATA AGCGCCGCGG	240

CCATTGGCCT	TGCCCCGTAGG	ATCAATAAAG	ACTTGTCCCT	CCTTGTTCTT	GACAATGCGG	300
AGCAAATCAC	GCTTATCAAT	CAC TTCGTTA	GACACAACAG	ACTTGCGCAA	AGGGATTTTT	360
CTTGTTTTCA	TCTTCCCTC	CTCTAGCAGC	TTTTATTCTT	CTACAGTATC	GTTTTCTACT	420
TCCAACCTCTA	CTGAAGCAGC	GTCTTCCATG	GCTTCAAATT	CGCTAGCAGA	CTTGATATCG	480
ATACGGTAAC	CAGTCAAGTG	AGCCGCCAAG	CGCACGTTTT	GTCCACGACG	ACCAATGGCA	540
AGAGAAAGCT	TGTTATCTGG	AACAACCACC	AAGGCACGTT	TGCTGTCGTT	TTCATCAAAG	600
ATAACTTGGT	CAACCTCAGC	AGGAGCGATG	GCATTGTAGA	TAAATTCAGC	TGGATCTGCT	660
ACCCACTCGA	TAACATCGAT	ATTTTCTTCG	ATTGGTACCA	TGCGGTCATT	TTTAGCATCG	720
TAACGAG						727

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAATGTAA	TCTATGGGAT	AAACGTTAGC	TTCTTTTAAT	AGATTATTAA	GCAATTTTTT	60
AAAACAAC	ATCAAACAAA	CTCAACTGGT	TATCTCTGGC	ATATTTCCAA	GAATACCCAT	120
CTCATCCATC	TTTTCAACCA	AGGTTGATGA	GAGTCCACCA	CGCTTGCGTA	GTTCTGTTTT	180
AGAGAGGAAT	TCTCCCTCTT	CACGCGCCCG	CACCAGTTGC	TTGGCAACGT	TCTCCCCCAG	240
ACCATCCATT	GCTACAAATG	GTGGGATAAG	GGTATCCCCG	TCGATGAGGA	ACTCTGTCGT	300
CTGACTACAG	TAGAGATCTA	ATTTACCAAA	CTTGAAACCT	CGTTCCCACA	TCTCATTGAC	360
AATCTCAAGA	GTTGTATAGA	GATCGATTTC	CACATTAGAG	GCTTCATTGT	TCTCCGTTT	420
TTCAGAGATT	TCTTCCATT	TGCGCTTGAT	GACCTCCAAG	CCCGCACCCA	TGGTCTTGAT	480
ATCAAAAGCC	TTAGCACGAA	TGGAGAAGTA	AGCACAGTAG	TAATAAATAG	GATGGTGAAC	540
CTTGAAGTAA	GCTACACGCA	AGG				563

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTAACTTCAA	AAGCTTTTAG	AATATCTTCT	TGACTAATCA	TATGATTACC	GCCCAAGGTT	60
AAGTTTTCCA	AAATAGAGCC	ATTAAAGATA	TAGGCTTGTT	GGGGTAGGTA	ATTAATATGA	120
CGGCGCAAGA	CTTTTTTTAT	CAATGTTTTT	AATATCCTGA	TGATTGATGG	AAATATGCCC	180
TTTGTAGGGT	TCAAAGAAAT	TGACAATCAT	TTTGGCTAAA	GTTGTTTTAC	CAGAACCACT	240
AACTCCAAC	AGGCTAACCT	TATCTCCTTG	TTTAATCGTG	AGATTAATAT	CTGTTAAGGT	300
ATCTCGTCCA	AAACCATACT	TATAAGAAAG	GTCATCAAAT	TCAATATCGC	CCATCAAAAA	360
ATGTGAATGA	ACAGGGTTTT	CTTGAACCTG	AAATTCAGAT	TCGACTAGAT	AGACTTCGTT	420
CAAACGGTTA	TTAGCGACCT	TCGCAGATTG	GAGTTTGGTT	TGGAGGTTGA	TAATATTTTC	480
CATAGGAGTT	GTAAAGTAAG	AAAGAAGTGT	GTTAAAGGTA	ATCAGCTGAC	CGATAGAAAT	540
TTTACTCGAC	ATGACTAATT	GAGCGCCAAA	CCATAGGATA	AGGATATTCA	GAAC TAATTT	600
TGTTTCCCCT	GCTTTAAACT	CGTTTGTAAG	ATAGAATATT	TACTGAG		647

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTATCCTNGA	ACCAATGATG	CTTGTAACAA	TCACTGTTCC	AGAAGAAAAC	CTTGGTGATG	60
TTATGGGTCA	CGTAACTGCT	CGTCGTGGAC	GTGTAGATGG	TATGGAAGCA	CACGGTAACA	120
GCCAAATCGT	TCGTGCTTAC	GTTCCACTTG	CTGAAATGTT	CGGTTACGCA	ACAGTTCCTC	180
GTTCTGCATC	TCAAGGACGT	GGTACATTCA	TGATGGTATT	TGACCACTAC	GAAGATGTAC	240
CTAAGTCAGT	ACAAGAAGAA	ATTATTAAGA	AAAATAAAGG	TGAAGACTAA	TCCGTCCTCA	300
CTCTAGAAGG	AAGTCACTTA	GTGGCTTCCT	TTTGCTTTTA	GAAAATACCT	CTAAATATGG	360
TAAAATAGTA	GAAGAATAAT	GTGAGGAAAA	TGAATGTCAA	ATAGTTTTGA	AATTTTGATG	420
AATCAATTGG	GGATGCCTGC	TGAAATGAGA	CAGGCTCCTG	CTTTAGCACA	GGCTAATATT	480
GAGCGAGTTG	TGGTTCATAA	AATTAGTAAG	GTATGGGAGT	TTCATTTCCT	TATTTTCTAA	540
TATTTACCTA	TTGAAATCCT	TTTTACAATT	AAAGAAAGTT	TGAGCGAAGA	ATTTCTTNAG	600
AANGCCATCA						610

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATAAGCATA	GTACCAGTTG	CCATTGACCT	GGAACCAACT	GTCTTCATAT	CTCCATTACT	60
GCATTTAGGT	AGTACCAAGT	TGAACCATCT	TGATACCAAC	CAGTTGCCAT	TGCTCCTGAT	120
GAACGGAGAT	AGTACCATTT	GTTCCCAAGG	TTTTGCCAAC	CTGTTTTCAT	ATCGCCATTT	180
GGCTGGTCTA	AATAATACCA	AGTGGTACCT	TCCTGATACC	AACCAGTTGC	CATTGCTCCT	240
GATGAACGGA	GATAGTACCA	TTTGTTCCCA	AGGTTTGGCC	AACCTGTTTT	CATATCGCCA	300
TTTGGCTGGT	CTAAATAATA	CCAAGTGGTA	CCTTCCTGAT	ACCAGCCAGT	GGCCATTGCT	360
CCTGAGGAAC	GGAGGTAGTA	CCACTTATTA	CCTAGATATT	GCCAACCTGT	TTGCATAATA	420
CCAGTTGTTG	GATCTAAATA	GTACCAAGTC	AAATCATCGT	TTATCCACCC	CGCACGTCTT	480
TCACCACCAA	GGTAGTTTTC	TCCATTAATT	TCCGTCTTAG	CTAGATAATA	CCAGTAGACT	540
GATCATAAAG	CCAACCTGTC	TCTAAAGAAT	GATTTTGATT	AAAGTAATAG	TTCGTATAAT	600
AACGNTTCTC	TTCTTTATCT	TCTGAATCTT	CACGTTTTTC	CCCGTACTTT	CTTCCAACAC	660
TGTCTTTAGT	TTTAATCTCT	AATGTTTTCC	AACCAACAAA	CTCTTGTAGC	ACTCCATTTT	720
TATCGAAGTA	GTACCACTCT	GAATTTGGAA	AACCTTCTAA	TCTCATACCA	TTTGGGTAAG	780
GACCAATTGT	ACTACCTTTA	GATGGAAACG	GGATATATTG	CCAGCCGACA	ACCATCTCTC	840
CAGATAGAGA	ATCAAAATAA	TAGTACTTAC	CATCAATCAC	TCGCCAGTAG	GTTTCTTTGA	900
GGTCCCCCTT	TTTGTAAATAG	GTTCTACCGT	TTTCTTGGAC	AAACTGCCAT	CCTTCAGAGT	960
TATCTGCAAA	TACTGTATTC	GTAG				984

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCTCGTTATG	CAGATGAACG	TTATTTCTTG	TCAAAGAGTC	ACAAGAATTT	TGTTGATCGT	60
AATCTTTTTA	TTACCATTCT	TGACAAGGAA	ACCACCTGTA	TCAAGCCTTA	TCAGCAGGAT	120
TTGGATTGTC	CACATGGTCT	GGCCTTGGAT	GTTTTCCTT	TGGATTATTA	TCCGAAAAAT	180
CCAGCTGAGC	GGAAAAACN	GGTTCGTTGA	GCCTTGATTT	ATTCACCTTT	TTGTGCGCAA	240
ACTATTCAG	AAAAGCATGG	TGCTCTCATG	AAATGGGGAA	GTCGCATTTT	ACTGGGTTTG	300

ACTCCAAAAT CTCTCCGTTA TCGCATCTGG AAAAAAGCTG AGAAAGAAAT GACTAAGTAT	360
GATTTGGCTG ATTGTGATGG CATTACAGAA TTATGCTCAG GTCCTGGCTA CATGAGAAAC	420
AAGTACCCAA TCACATCTTT TGAAGACAAT CTTTCTTGC CATTTGAAGG AACAGAGATG	480
CCTATTCCAA TCGGCTATGA TGTCTATCTC AGAACTGCTT TTGGGGATTA TATGACGCCT	540
CCACCAGCAG ACAAGCAGGT ACCGCATCAG GATGCTGTCA TCGCTGATAT GGATAAGTCT	600
TATACAGAAAT ACAAGGGAGA ATATGGTGGC TAAGAAAAAA ATCTTATTTT TTATGTGGTC	660
TTTTTCTCTT GGAGGTGGTG CAGAGAAGAT TCTATCAACC ATTGTTTCAA ATCTGGATCC	720
AGAAAAGTAT GATATTGATA TTNTTGAAAT GGAGCACTTT GACAAGGGAT ATGAATCTGT	780
TCCAAAGCAT GTACGCATTT TAAAATCCCT TCAAGATTAT CGCCAAACCA GATGGATACG	840
AG	842

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTGGCAAATA CAAGGTGACG ATCATTGGTA AATCAGCCCA CGGTGCTATG CCTGCTTCAG	60
GTGTCAATGG TGCGACTTAC CTAGCCCTCT TCCTTAGCCA GTTTGACTTT GCTGGTCCAG	120
CCAAAGAATA CCTTGACATC ACTGGTAAAA TTCTCTTGAA CGACCATGAG GGTGAAAGTC	180
TCAAGATTGC TCATGTGGAT GAAAAGATGG GTGCCCTTTC TATGAATGCA GCGCTCTTCC	240
GCTTCGATGA AACAAGTGCT GATAATACCA TTGCCCTCAA CATCCGCTAT CAAAAGGAA	300
CAAGTCCAGA ACAAATCAAG TCAATCCTTG AAAACTTGCC AGTTGTTTCT GTTAGCCTGT	360
CTGAACACGG TCACACGCCT CACTATGTTG CCAATGGAAG AATCCACTTG GTTGCAAACC	420
TGGTTGAAAT GTCTATGAAA AACAGACAGG CCTTAAAGGT CATGAACAAG TCATCGGTGG	480
TGGAACCTTT GGTGCTTGT TAGAGCGCGG AGTTGCCTAT GGTGCTATGT TCCCAGACTC	540
AATTGATACC ATGCACCAAG CCAATGAATT TATTGCCTTG GATGATCTCT TCCGAGCAGC	600
AGCAATTTAT GCCGAAGCTA TTTACGAATT GATCAAATAA AACGATAGAA GTCTGAGATC	660
TTATGCTTGG ACTTCTTTTT GGAGGGAAAG TAGATGTCTC AAATCGAAAG AATCAAACAG	720
GCTATCATGG CGGATTCACA GAATGCCAG	749

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGGATGAAT TGCAGAAGCG CAACCTACTG GGATTTGTCT TCCAAGATTT TCAACTATTT	60
CCTCATCTAT CAGTTCTGGA AAATTTGACT TTATCGCCTG TGAAGACCAT GGAATGAAG	120
CAGGAAGAGG CTGAGAAGAA GGCGAGTGGA CTCTTGGAAC AGTTAGGACT AGGAGGACAC	180
GCAGAGTCCT ATCCTTTCTC ACTATCTGGT GGGCAAAAGC AGCGGGTGGC TTTGGCGCGT	240
GCTATGATGA TTGACCCAGA AATCATTGGC TACGATGAAC CAACTTCTGC CCTGGATCCA	300
GAATTACGTT TGAAGTGGA GAAGCTAATC TTGCAAAATA GGGAACCTGG GATGACCCAC	360
ATTGTGGTTA CCCATGATTT GCAGTTTGGC TGAAAATATC GCACATGTTA TTATTGAAAG	420
TAGAACCTCA AATAGGAAGA AAAATGGATT GAAAAAATGG ATGCTTGAT TAGTCAGTCT	480
GAAGACTGCC TTTGTTCTTA GTA	503

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTGGAGGGCA TTCAGTATTA CTTGAATAGA GGAAAACATC ATCTCCCTTA TGTTCTCAAT	60
ATTGGATTTT CTGGTCAGAA AAATGACCTC TTACTCCTTC GGCTAGATTT AGCTGGAATT	120
TCAATCTCTA CTGGCTCAGC CTGTACTGCA GCGGTTGTCC AATCCAGCCA TGTTCTTAAA	180
GCCATGTATG GCGCAAATTC AGAACGCTTG AAGGAATCCC TTCGCATCAG TTTGTCGCCA	240
CAAAATACCG TTGAAGACCT ACAAACCTC GCAAAAACCT TAAAAGAAAT TATCGGAGGT	300
TAGCCATATG GCATTTGAAA AAATCATTCA GTTAAAAAAT TGTCGTTACG ATTACACTCT	360
TAGCCCTTCT GTTAAAAAAT TCACCCTCAA AGATAACACC TTTTGTGAAA CTAAGGTTGG	420
TAACATGAA CTGACTCGCC TTTTGGAATA AGTGCCAAAC AGCGGTGAAG GCTTCCAACT	480
CAAAATCATC ATTAACAAGG AACTTACAGG GGCTAAATC AATATCACTG ACAAGTTTGG	540
CCTTCGTCTA GTTGATATTT TCAAATCAGA AGACCACCAT ATTCATCAGG AAAAATTCTA	600
CTTCCTCATG GATAG	615

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 954 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTGCAATGGT TAGCGAGGAT GGTGAAATAG AGGAGCCTTA ACTATTTTGA GGAATCCAAG	60
CTGACAGGAC TGGTATGTCT GCTCTTTGGC TCTGAAGGCA GACTATACCA GCTGGAAGTT	120
TGACAGATGT GGCACGTGAG AATTATTGGA GGCNTTGACN TANTCAGAGG ATTCTCTCTT	180
GATATTGGGT TTGGCAGAGT TGGATAGTGA GTTGGAAAAT TACCAAGCGG TTATTCAAGC	240
CTATGCCCAG TTAGATAATC GCTCGATTTA TGAGCAAACG GGCATTTCCA CCTATCAACG	300
AATTGGCTTT GCCTATGCTC AGTTAGGGAA ATTTGAAACG GCTACTGAGT TTTTAGAAAA	360
AGCCCTGGAG TTAGAATACG ATGACTTAAC AGCTTTTGAG TTGGCCAGTC TTTATTTTGA	420
TCAAGAAGAA TATCAAAAAG CCACCCTCTA CTTTAAGCAG CTTGATACCA TTTCTCCTGA	480
CTTTGAAGGC TATGAGTATG GGTACAGTCA GGCTTTACAT AAGGAACATC AAGTTCAAGA	540
AGCCCTGCGT ATCGCTAAGC AAGGATTAGA GAAAAATCCC TTTGAACTC GCCTCTTGCT	600
AGCTGCTTCA CAATTTCTT ATGAATTGCA TGATGCTAGT GGTGCAGAAA ATTATCTCCT	660
TACTGCAAAA GAAGACGCTG AGGATACAGA AGAAATCTTG CTTCGTTTAG CCACTATTTA	720
TCTGGAGCAG GAGCGTTATG AGGATATTCT AGACTTGCAG AGTGAGGAGC CAGAAAATCT	780
TTTGACCAAG TGGATGATTG CTCGTTCTTA TCAAGAAATG GACGATTTGG ATACTGCTTA	840
TGAGCATTAT CAAGAGTTGA CAGGAGATTT GAAGGACAAT CCAGAATTTT TGAACACTA	900
TATCTATCTC TTGCGTTGAA TTGGGACATT TTGAAGAAGC AAAATCCCAT GCTC	954

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTATGAAACA TTTTGATACT ATTGTCATCG GTGGGGGACC TGCTGGTATG ATGGCTACGA	60
TTTCCAGTAG CTTTATATGGA CAGAAAACCC TCCTCATCGA AAAAAATCGG AACTTGGA	120
AAAAATTAGC TGGGACTGGT GGGGGACGTT GCAATGTGAC CAACAATGGT AGCTTAGACA	180
ACCTGCTAGC TGAATTCCCT GGAAACGGAC GCTTCTTTA CAGTGTTTTC TCCAGTTTCG	240
ATAATCATGA CATCATCAAC TTTTACAG AAAATGGTGT TAACTTAAG GTCGAAGACC	300
ACGGACGCGT CTTTCCAGCC AGTGACAAGT CTCGGACTAT TATCGAAGCT TTGGAAAAGA	360
AAATCACTGA ACTAGGTGGT CAAGTTGCTA CTCAAATAG AAATCGTTTC TGTTAAAAA	420
GTAGATGACC AGTTTGTCTT TAAGTCAGCG GATCAAACCT TCACTTGTGA GAACTCATT	480

GTCACAACAG GTGGTAAGTC TTATCCTTCG ACTGGTTCGA CTGGTTTGG TCACAATGCT 540
 CCGCCATTTA AGCATACCAT CACG 564

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCCGTGGTC TTTTGGTTTG CTACGGGATG TAGGCAAAAG GCAAGTCCAT TTTATCAGCA 60
 ATAATGGCTC CGTGTGGAAT CCCTGCTGTT GCAGTTCCTG CAATCACTTC TACTTCAGGA 120
 AAGGCTTCTT TGATAGCTTC CACAAAACCA TTTTCAATTA GGGTACGAGT TTCTGGATAG 180
 GCTAGTGTCA CACGATTATC AGTGTAATC GGTGACTTGA TACCAGATGC CCAAGTGAAG 240
 GGTTCCTCTG GTTTGAGGTA AACGGCTTGG ATTTTCAAGA GGTGGCTAGC GATATCTTTA 300
 GCAAGTGTCA TGGTATTCTC CTTTTATTTT TCTAATCTAG TTCTTTAATT CCAGTCCTGT 360
 GTCCATTTCAT CCTTGATGGC ATGATAAGCT GCAACAGGAT CCTCAGCTTG GGTAAATGGGA 420
 CGTCCCACTA CGATATAGTC ACTGCCGATT TGATAGGCAT CAGCAGGTGT CATGACTCGT 480
 TTTTGATCTC CAACTGCAAC ACCAGCTGGA CCAATCCCTG GTGTCCCGAC AGATAAAAAT 540
 CTGGATTGGT AGCCCTGCTT GATGACTTTG TCACTTCCCT GAGCCGAGCC AAACCAACAC 600
 CCATCCCAAA GCCCAAGCTT CAGCTGTCTT CCTTGGCATA GTTGAATCCA C 651

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTAGTATCT AGAAAAGGAG AAATAAAATG GTTAAAGTAT TAGCAGCGTG CGGAAATGGA 60
 ATGGGTTTCAT CAATGGTTAT CAAGATGAAG GTTGAAAATG CTCTCCGTAA GCTTAATCAA 120
 ACAGATTTTA CAGTCAATTC ATGCAGTGTC GGTGAAGCTA AAGGTTTAGC AGTAGGATAT 180
 GACATCGTAA TCGCTTCTCT TCATTTGATT CAAGAATTGG AAGGGCGAAC TAATGGGAAG 240
 TTAATTGGGC TTGATAACTT GATGGATGAT AAAGAAATCA CCGAAAAACT CAGTCAAGCA 300

ATACAGTAAA	AGGTTGGAGG	GGGCTGGACA	CAAACTGAGA	GTTATCGTTT	CTGTCCTTCT	360
CCCTCTTTAA	ATAAAGGAGG	CAGATATGAA	TTTAAAAACA	GCTTTAATTG	ACAACGACTC	420
GATCCGACTA	GGTTTAGAAG	CTAACGAATG	GAAAGAAGCA	GTCAAGGTAG	CAGTAGATCC	480
CTTGATTGAA	AGTGGGGCAA	TTTGGCCAGA	GTATTACGAT	GCTATCATTG	AATCGACTGA	540
AGAGTATGGG	CCTTACTATA	TCTTGATGCC	AGGTATGGCT	ATGCCCCACG	CTAGACCTGA	600
AG						602

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGGGAATT	TTTGCAACTG	CAATTGGTGC	CCTCAGTAAT	CTATAAAATA	GATTCAAGAA	60
AATTTAGTGA	CTGGGATTTC	CCAGCCCTTT	TTTAAAGTGA	GAAGAAATAA	TGAGTATGTT	120
TTTAGATACA	GCTAAGATTA	AGGTCAAGGC	TGGTAATGGT	GGCGATGGTA	TGGTTGCCTT	180
TCGTCGTGAA	AAATATGTCC	CTAATGGAGG	CCCTTGGGGT	GGTGATGGTG	GTCGTGGAGG	240
CAATGTGGTC	TTCGTTGTAG	ACGAAGGACT	ACGTACCTTG	ATGGATTTC	GCTACAATCG	300
TCATTTCAAG	GCTGATTCTG	GTGAAAAAGG	GATGACCAA	GGGATGCATG	GTCGTGGTGC	360
TGAGGACCTT	AGAGTTCGAG	TACCACAAGG	TACGACTGTT	CGTGATGCGG	AGACTGGCAA	420
GGTTTTAACA	GATTTGATTG	AACATGGGCA	AGAATTTATC	GTTGCCCACG	GTGGTCCGTG	480
GTGGACGTGG	AAATATTCGT	TTCGCGACAC	CAAAAAATCC	TGCACCGGAA	ATCTCTGAAA	540
ATGGAGAACC	AGGTTCAAGG	ACGTGAGTTT	ACAATTGGAA	CTTAAA		586

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TTCGACAATC	TTGCCCNGA	TCCAAGACAA	CCAATTCTCT	GTCCGCTCAG	CAATAGTCAA	60
GCGGTGAGCA	ATGAAAATCA	AAGGTCTTGT	CCAAAGCCAT	GAGATAATGG	ACAATCCGTT	120

TTTTTGTCAA AATATCCAAA CTGTTAGTCG CCTCATCCAA AATCAAGACC GGCGCATCTG	180
TCAAGAGAGC ACGCGCCAAA GCGATTCTCT GACGTTGACC ACCTGAAATC CCTGCCCCAT	240
CCGAAGTCAA TTCTGTCTGG TAAATTTCAA GGTGGCATGG CGGCTTCGAG ATATTCCTCT	300
TCGGAATCTC TGAACCAAAT TCGGACCGGC CCGTTAAAGA TATCTCCCT GTGTCGTCCC	360
CTCCCTTGGC TCCCAAAAGA AGATTCTCCA AAATCGTTCC GTTAAAGACA TAGGGCTGTG	420
GAGGCAGATA GATGATGTAC TGGCGTAGGG CTTTTTTATC AATCTGATTG AGATTGACAC	480
CACCCAGACT AATCTCCCCT TGAATTGGGT CGTAAAAATT AACCATCATC TTGGCCAAAG	540
TCGTCTTACC TGACCCTGAA ATCCCCACAA AAGCCACCTT AGACCCTTGG GGAACGGTTA	600
AATTGATATC CGACAAGACG TCTCGACCAT AGCCATACTT GTAATGAACC TGCTTGAAAG	660
TCATCTCTCC CTTCATCAAG	680

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCAATTTGGA TTTGCGAGAA GGCGTTATTA TTTCAGATGC TGGTTCGACC AAGTCAACCA	60
TTGTGGATGC GGCGGAGCAG TATTTGGCTG GCAAGTCTGT TCGCTTTGTC GGGGCCCATC	120
CCATGGCTGG TAGTCACAAG ACAGGGGCTG CTTCCGGCAGA TGTCAATCTT TTTGAAAATG	180
CCTATTATAT CTTTACAACC TTCCAAAGCC CTGAACAAGT CAAGGACAAC GCTTAAAGGA	240
AATGGGAAAG GATCTGCTTT CCAGGTCTTC ATGGCTCGTT TTATCGAGAT TGATGCCAAG	300
GAGCATGATC GTGTCACTTC TCAGATTAGC CATTTTCCTC ATATTTTGGC TTCTAGTCTC	360
ATGGAGCAGA CTGCGGTCTA TGCTCAAGAG CATGAGAATG GCAAGGCGCT TTGCGGCAGG	420
TGGTTTTCGA GATATGACCC GAATTGCGGA AAGCGAGCCA GGAATGTGGA CCTCCATTCT	480
CTTGTTCCAAT AGCGAGACCA TTCTGGATAG AATTGAGGAT TTCAAGGAAC GTTTGGAAGC	540
GATTGGTCAG GCCATTAGTA AGGGAGATGA AGAGCAAATT TGGAACTTTT TTAACCAAGC	600
G	601

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGGCTCATC	AGGGGCAGGA	TATTTATGAT	TTCCCTCGTG	CTATGATTAA	GGAAGATAAT	60
CTGGAGTTTT	CATTCTCTGG	TTTGAAATCT	GCCTTTATCA	ATCTTCACCA	CAATGCCGAG	120
CAAAAGGGAG	AAAGTCTGTC	TACAGAGGAT	TTGTGTGCTT	CCTTCCAAGC	AGCTGTACTG	180
GATATTCTCA	TGGCAAAAAC	CAAGAAGGCT	TTGGAGAAAT	ATCCTGTTAA	AACCTGGTT	240
GTGGCAGGTG	GTGTGGCAGC	CAATAAAGGT	CTCAGAGAAC	GCCTAGCAGC	CGAGGTTACA	300
GATGTCAAGG	TCATCATTCC	ACCTCTGCGC	CTCTGCGGAG	ACAATGCAGG	TATGATTGCT	360
TATGCCAGTG	TCAGCGAGTG	GAACAAAGAA	AACTTTGCAA	ACTTGGACCT	CAATGCCAAA	420
CCAAGCCTCG	CTTTTGATAC	CATGGAATAA	AGAGTGGCTC	TTTGTCAAGT	GTAGTGGGTA	480
GGCGAAAAGC	TACAATCTGG	AGANTACGAA	ATTC			514

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTTGGATTAT	AAAATACAAT	CGGCAAGATC	ATAAGTCCCA	AGCCTAAAAA	TATATAGAAA	60
GGGGGTCACC	TTCCAAAGAA	ATTCTGTATT	AAAGAGCATG	ACCACAAAAC	CAATCACAAG	120
CCCCAAGGCA	ATCCAGGCGA	CCTGCTGCCC	TAAATGGGC	AGAATATTAT	TGGGGTAATC	180
ATGACTAACG	GCTATATAGA	TAGCCACCAC	ACCGATGACC	AGTAGAAAAA	ATACTGGCAA	240
GAGCAAACCTG	TAATCGACTC	TTGAGTCGAG	AGAACGTTTC	ATATAAACTA	ACCTTATACT	300
TTCATACAAT	ACTATTTATC	AAAGTTCATT	AAAAAATCTA	TCAATAGCCT	CGTCAACTTC	360
GGATCGAGAG	ATGGTTTTAA	CAGTCGCTTC	TTCTGCTAGA	GATGCTACTA	TTTGTTTGCC	420
GTATCGTTTT	CCGACGATTC	TCCTATCCAA	AATAAGAGTT	AAGGAACGTT	GGTATTCACG	480
TCTCATACTT	CTTCCCAAAG	CCTGTTTTAA	ACGAATAATG	G		521

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTGCCTGAT GACATCATTG ACTCTTTTGT GTATATCATC GACCATTCTT TAAAAAATGT	60
CTTTGAATTG GAAGAAGAAC TCGAGTTTCA ATTGCTTAAT AACCAAGGAA AGATTACCTT	120
CCACTTTTCA AGTCAACACC TCCCTACAGC CATTGATTTT GACTTTAACC ATCCTTTCGA	180
CCCTCGTTAT CCCCCAAGAG TACTGGTTTT AGACATGGAC GGTAGAGAAA CTATCCTCCT	240
CCCAGAAGAA AATGACCTAT TTTAAAAACT CTAGCCTTCA GTTGCAAGTG ACTGAAAACT	300
AGAGTTTTTC TATTTTTTCA AAGCATCATA CAAGTTGCGG ATCGGTTGTT TTAATATCGG	360
ATGGATAAAA TGAGGCGCAA TTTCCTGTAA GGAACAAGG AAAAAAGGC GTTCCCGCTA	420
TGTTAAGGGA TGAGGCAATA TGAGGTCGTC TGTATAAAGG ATCTGGTCCT CCCACAAAGA	480
GCAAGTCCCA AATCAATCCA AACGAAGTCC CCCAATGCAC TTCTCTCACC CGTCCCCAGC	540
TCTTGACTCC AATGGCTAAC AAGGTTTCNT AACAAATCTT GTTGCTGGTA GCCAAGTTC	599

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTATGGGTAA AAAGGATGCC TCTGCTATGC ATGAGATGAG GGCTTCCTTT ATTCAAGGCT	60
CCATAGAAGC AGGCCATACT GCGGAAAAAT CAGAGCAGGT TTTTGATGTT ATGGAGAAGT	120
TTGCAGGTTA TGGATTTAAT AGATCTCATG CCTACGCTTA CTCAGCCTTG GCCTTCCAGT	180
TGGCTTATTT CAAAACGCAT TATCCAGCCA TTTTATATCA GGTCATGTTA AATTATTCCA	240
ACAGTGATTA CTTAATAGAT GCACTTGAAG CAGGTTTTGA AGTAGCCTCT CTATCCATCA	300
ATACTATTCC CTATCAGAT AAAATTGCCA ACAAGTCTAT CTATATAGGT TTGAAATCGA	360
TTAAGGGGCT CCAGCAAGGA CTTGGCGCTT TGGATTATTG AACATAGACC TTATTCTAAC	420
ATTGAAGATT TTATAGCTAA ATTACCTGAG AATTATCTGA AACTTCCTCC TGCTAGAACC	480
TTTGGTAAAA GTTGGTCTTT TCGATTCAAT TGAAAAAAT CGTCCAAAAG TATTTAATAA	540
CTTAGCTATC TATTGAATTG TGAA	564

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACTAATCACT	TACTACGTAG	CTTCTGACTA	TCTACCTCTA	CTAGATAAAG	GACAAACTGT	60
AAGATTAAAA	CTGGAGAAGN	TTGGAAATCA	CGGCATTACC	ACCATCGGCC	AACTTCAGAC	120
AATTGATCAA	ACTCCTACCA	GAACAGAGCA	AGGCAATCTC	TTTAAATTAA	CCGCTCTTGC	180
AAACTATCT	AATGAGGATA	GTAAACTCAT	CCAATATGGC	TTACAAGGTC	GCGTCACTAG	240
TGTAAGTGCA	AAGAAAACAT	ATTTTGATTA	TTTCAAAGAT	AAAATTTTAA	CCCATTTCTGA	300
TTAATTTTCA	GATAACACTC	TATAACTATT	TATTATCTTA	TCAAAAAGGA	GAATCATAAC	360
ATGGATAAGA	AACAAAACCT	AACTTCATTT	CAAGAACTAA	CAACTACCGA	ACTCAACCAA	420
ATTACAGGTG	GAGAATGGTG	GGAAGAACTC	TTACATGAAA	CAATTTTAA	TAAATTTAAA	480
ATCACAAAAG	CAC TTGAACT	ACCTATTCAG	CTATAAAAAC	AAGACCGAGA	AACAAGAACT	540
CTCGGTCTTG	TTTTTTATCA	TTCTGCATGT	ATCACAGTAA	GTACCTGACG	AAAGACTTGA	600
TTTGGCGAG	G TAGTATT					618

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAGGGGATGC	CAGTTGATTT	GCTTCAAGTT	GACTTGACTC	GTACTTGGA	AATCCTCGGA	60
GAAATCACTG	GGGATGCTGC	TCCAGATGAA	CTCATCACC	AACTCTTTAG	CCAATTCTGT	120
TTAGGAAAAT	AAGAAAAATC	CATGATCCTT	CATTGCGTCA	TGGATTTTAT	TGTCTTTATT	180
AGTAATCTGG	TCTTAAGACC	CCTGTTACAG	TTGCCTTAGT	TGCTTCGTAG	TCGCCATCTA	240
CGACAACCTT	GATAATGCGT	TTGACATCTT	CTTCTGGTGC	TGGAACAAGA	GGTAGACGAG	300
TGGGTCCAGC	TTCAAATCCC	ATATAGTTAA	GAATTGCCCTT	AACTGGAGCA	GGACTTGGAT	360
AAGAGAAGAG	AGCATTAAAC	TTAGGAATGA	ATTTACGCTG	AATTGCTGCG	GCTTTCTTCA	420
TATCGCTTTC	TGCAATGGCA	GTAAACATCT	CGTGCATTTT	ATCCCCATTT	GTATGAGAAG	480
CAACAGAAAT	AACCCATCCG	CCCCAAGGTT	CATGGCATGG	AAAGCATCTC	CATCCTCACC	540
TGTATAAAT						549

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
CTGGCTANCA AAATCATACT CATAATCCTT AACACCGACA GAGATAGAAG CAATGAGCCC      60
TTGATCGTGC ATTCGTTTAA TAAAAGGAAT GCGTCCTGCC TCATCAAAAC GGTGCATAAG      120
TGTACAAGTA ACCACCTTTA GCCAGTTGCT CTGCTACATT TTCATCCAAA ATCGTCTGCA      180
TATTCGCTGG CACAACAGGT AGTTTAAAGG TGTGATTTC TAAAGTGACA CTTGTATCCG      240
CTTCTGCACG GCTTTTAATG ACACATTTAT TTGGAATCAA TTGAATATCT TCGTAATCAA      300
AAATTGGAAG TTCATTTAAC ATATCGATGT CTCGTTTCTT TTGTAATGAC CTACCTATGC      360
TCTCGCATCA CTACGCCTTT TCCGACGTTT CCCTTAAATT TATTATAAAC CAAAAGTACA      420
GTTTTTGTCA AATTATTTCA TGAATNAAAT ATATC                                     455
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
CTCCTGGGTT TTGATTAACT CTAGGGTTGC CAAAAAGAGG GTGATGACTT CTTGGACATT      60
CTGGGCTTCC TTGAACAAAT CCTGCAAGCG CAATTGATTT CGTCCAATCA AGGATTCTTT      120
CACAATAATC ATCATGTCCT CAATCTTATA CTCATCCCGC AAGATAGTCG TGTGATTTTG      180
TGCAAACTCC TCTTTTTTCT TGGCTAGGAT ATTTGAAAAA GCCAAAAAGA GGTCATGGT      240
CGTCTTGTC TGCACAAGCT CCGCATCTTC GTAAATCAAC TCTATCGGCG CTTTGAATA      300
ATACTGGGCC CGTTTCTTGG TGCTTGGCTT CCAAGTGCTC ACCCAAGAGC TTGAACTTGC      360
GATATTCTTC GATTGAGAG AGGAGGTCCT GCTCCAGGTC ATCCCCAAG TCTGTCACTT      420
CTGCTACCTT CGGAAGGAGT TTACGACTCT TAATCAGCAT GAGCTGACTA GCCATGACCA      480
TGTA CTACC CGTCACTTCC AGACGCATGG CCTGCAGGGT TGAGACATAG GCTAGATACT      540
GTTTCGATGAC TTCCGTAATG GGCACATCGT AGATATCCAT CTGGTACTTA GAAACCAGAT      600
GCAAGAGTAA GTCCAGGGGT CCTTCAAAAT CTTTTAATTT AATATCCATT ATCTATATTT      660
TTCTAAGGTC AGGACTGTTT TTAATCCTAA TTTTTTTGCA ATTCGTACA AATCGACCTT      720
GTTTTCTATT TGTCTTAGA ATAACTGTT CACGTAAGAC TTGAGATCGA ATTCCT      776
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

ATTGATACCN ATTGTACAGG ACAACTTATT TTGGAGCGCC ATAGCAGGGA TANGGTTAGC      60
AATAGATGCG NTGACCATAG AAACGTTTNT TAGCCAATAC ATAACCTGCT AGAGATGAGG      120
TTGCACAAAC TAAGAACATG GTTACCAATG AGATAAATAC TGAGTTCCAC ATCCATTGCA      180
AGGCAGGGTT CTGCACCATG AGTTGTTGGA AGTTTTCAT GGTGGCATT TTAGGGAACC      240
ACTGAGGAGG AATAACAATT GTATCAGGTT GTGATTTGAA TGCCCTGTC AAAATCCAGT      300
AGAATGGAAA GATGNACAGC ACAGTCAACA AGAGCAAAAT GATTGTTGAA ATNACAGTAA      360
AGGCTGTAA TGGTPTTTTT TCTGTAGATT GCATAGCTGT CTCCTTCTT TAGTATTCTA      420
CGTCGTTTCC AAGTACTTTA AATTGAACAA AGCTTACGAT AGCAATCATG ACTGCCAAGA      480
AGACACCAAT TGTGTTGGCA TAGCCGTATT CTGTCAATTG GAAGGCTTTT TCGTAAAGGT      540
AGTACATCAA GGTACTTGTT GAGTAGTTTG GACCACCAGA TGTCAAAGC TGAATCAAGG      600
CGAAACACTG GAATGAGTTA ATTGTTGTGA TGATTGCAAT ATAAAGAGTT GTTGGAAGAA      660
GGCTTGGCCA TTAAATCTTC CAAAAAATT GAAACTCAGT TGCACCATCA ACACG      715

```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

CTGGGCTGAG TTTTCCAGAT ACAAATACTG CAACCGCAAC TGCAATCCCC CAACCCATAG      60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTTGG AAGAACCACA CCTGCAACAA      120
CACCATTTC TAGAAGAATC AGGATTAAAG TCCCTAAAAA TTCTCCAAAT AATTCACTCA      180
TCATTTTCT GTCTCCATTA AAAAGAAGGG GCGGGCGACA AGGATTGCTA CCCTCCACCT      240
CTTTTATTT TTCTTAATT TTAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGCTTTTA      300
CATCAGCAG GTAAGTTGCT TTTTCTTCT CTGTCCAGTC ATAGAATCGT CCCATTTTCAT      360
CCAAAACCTG CTCAACGATA CTATCCAAGC TATCACGCAT AAAGAGCATG TGATTGGTAC      420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG      480

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CTTAATTATA ACTTAAACAC AAAAGTTTTA CACAACTGT GGATAACTCT TTTGAAACTG      60
TGATTTTCTT AATTGAAATC TATTTTATAT TTTGTGAATA AGATGTGAAA AAATAGAGAA      120
TATGTTAGAA TAGAGTCATG AAAATTAAAG TTGTAACAGT TGGGAACTG AAAGAAAAGT      180
ATTTAAAAGA TGGTATCGCA GAGTATTCAG AACGAATTTC TAGATTTGCT AAGTTTGAAA      240
TGATTGAGTT ATCAGATGAA AAAACACCAG ATAAGGCCAG TGAATCAGAA AATCAAAAGA      300
TTTTAGAAAT AGAAGGTCAG AGAATTTTAT CAAAAATTGC TGACCGTGAT TTCGTTATTG      360
TGTTAGCCAT TGAAGGGAAA ACTTCTTCT CAGAAGAATT TAGTAAGCAG TTAGAAGAAA      420
CTTCTATAAA AGGANTTTCT ACTCTTACTT TTATTATTGG GGGAAAGTTT GGATTGTCAT      480
CATCTGTAAA AAATAGAGCC AATCTTCTG TCAGTTTGG TCGCCTAACC TTGCCTCATC      540
AGTTAATGAG ACTAGTTCTT GTTGAACAAA TCTATCGCGC TTTTACGATT CAGCAGGGAT      600
TCCCCTACCA TAAATAGAGA ATTGACTTTT AATTGAATTT TTGGTAGAAT AATTGTGTGA      660
GGTCTCATAG

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

CTATAATTTT ATTAGCTGTA TTCCAGTCGT CACGACCAA CTCTGTTACA GGGACACGAA      60
TGTCAAAACG GTTCTCAATC TCCACAATCA ACTCAACCGT TCCCATACTA TCCAAGACAC      120
CTGCATCAAA AAGATCTTCA TCCATCATGT CAGAAACATC TTCCATAAAC AACTCATCAA      180
TAATTTGAT AACTTCTGAT TTGATATCCA TATTTTATTT CCTTTATTT TTTAAACCAT      240
AGATTATTCA AGAATCCAGA AAAGATTAAG AATGACAACA TGACAACATG GAAAGTGACA      300

```

ACCATGCCAA	GCAACTGAAT	CCAGCGATTC	TCAGGTAGGG	CAGCCTTCCC	TGCTTTTTTC	360
CGTTCCTTAT	TGAGCGTTTT	TTTCTTGCGA	ACCCAGGCAT	CATTGATGAA	CAAGCCTAAG	420
TCCATGAAAG	AGTCCCATAG	GCGATATAGT	ACCAGGTCAC	ACCATGCCAA	AATCCCCATA	480
ATCCAGCATA	TTTACAATGT	AAGATC				506

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGGTTTCGAC	CCACAAATAT	GTTTTGCGAA	TCATTGACCA	TTCTATGATT	TACGTTGCCA	60
TTGCCGGCTC	ATACACGCCC	GTTGTCTTGA	CCTTGATGAA	TAAGTGGTTT	GGCTATCTGA	120
TTATTGTCAT	CCAATGGGGA	ACGACCATCT	TTGGTATTCT	CTATAAAATC	TTTGCTAAAA	180
AGGTCAATGA	GAAATTTAGC	CTTGCTCTTT	ACCTGATTAT	GGGCTGGTTG	GTTCTGGCTA	240
TCATTCTGTC	CATTATCAGT	CAAACNACAC	CCGTTTTCTG	GATTCTCATG	GTAAGTGGCG	300
GACTCTGTTA	TACAGTTGGA	GCTGATTGAT	AGCCTTTATG	CATTGAAATT	TGACAGTTTG	360
ACTTATGAAA	ATAAAGCAGA	GGTTATGGAC	TTTATCAAGG	CTCGTGTGTA	TAAGATGATG	420
GGCTCTACTC	CAAAAGATAT	CAAGGGAAGC	AGTTCCTGCA	GGTTCAAACT	TTGTTGTGGC	480
AGATATGTTT	GGAAGCAGCA	AGTGCTCTCG	TAGAAGTAAG	CAAGGAAGAA	GATTTTAAAC	540
CATCTGTTGA	ATCACTTTCT	CGTGCCTTTA	ACCTGGCTGA	GAAGGCAGAA	GGGGTTGCTA	600
CAGTTGATTC	AGCACTATTT	GAGAATGACC	AAGAAAAAGC	TTTGGCAGAA	GCAGTAGAAA	660
CACTCGTTTT	ATCAGGACCT	GCAAGTCAGC	AATTGAAACA	ACTCTTTGCC	CTTAGCCCAG	720
TCATTGATGC	TTTCTTTGAA	AATACTATGG	TAATGGCTGA	AGATCAGGCT	GTCCGTCAAA	780
ATCGTTTGGC	AATCTTGTC	CAACTAACCA	AGAAAGCAGC	TAAGTTTGCT	TGTTTTAACC	840
AAATTAACAC	TAAATAAAAT	TTGATAAACG	GACTTTATCT	TATTACAAAG	GAGAAGAAAT	900
GGATCCGAAN	ANATTGCTCG	T				921

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

CTTGCAACA GGCTCTTTTT GTATTGCGTT TATTAAGAAA AACAAAAAAC ATCGATATAA    60
CATTTAACTA AAAATTATTG TATGTTATCT CCCTTAATTA GGAATGATAA GGAATAACT    120
AGAAAGATTT GTGAATACAA ACTATTTCTG ATATACAAAA TATACAGTAA TAATGAATGA    180
TGGGAGATGG GATGAAAGAA TTTCAATTG AGAGAAAGCA GCGTTTTTCT TTGAGGCCAT    240
ATGCAATAGG AGCTTGTTCT GTCTTGCTAG GAACGAGTTT ATTTTTTGCT GGTATGGGTG    300
CTCAGCCTGT ACAGGATACA GAAACGAGTT CAGCACTAAT TTCAAGTCAT TATTTGGATG    360
AGCAGGATTT ATCTGAAAAG CTGAAATCTG AGTTGCAATG GTTTGAATTA GAAAACAAGC    420
TTTGAACCTT ATGGGAACAT TAGGTTACTA TGAAGGATTT GTTCCTTATG TTTCAAATCA    480
ATACAAAAAC CAAGCTGAAG AAGAAGGCAA ACCGCTATCT GATAAATATA TTTTCGAAAA    540
ATCTTAAGAA AACATATGC ACCTTCAAAA A

```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

GTATCAACTC CAAAGAGCAA GTGACTGTCA AAGTTGTAAC AGATGCGGCC AAGAAGCTCA    60
TGGGTGATAA GATTGCTCGC CAGAAAGAAC GTGGGATTCA GATTGANACC TTGCGNACCA    120
TGATTATNGG GATTCCANAC GNTGGTAAAT CCACTCTGAT GAACCGTTTG GCTGGTAAAA    180
AGATTGCTGT TGTGGAAGAC AAGCCAGGGG TCACAAAAGG TCAACAATGG CTTAAACCA    240
ATAAAGATCT GGAAATACTT GGATACACCG GGGATTCTCT GGCCTATAGT TTGAGGATGA    300
AACTGTTGCA CTTAAGTTGG CATTGACTGG AGCTATCAAG GATCAGTTGC TTCCTATGGA    360
TGAGGTTACC ATTTTGGTA TCAATTATTT CAAAGAACAT TATCCAGAAA AGCTGGCTGA    420
ACGCTTCAAA CAAATGAAAA TTGAAGAAGA AGCGCCTGTG ATTATTATGG ATATGACCCG    480
CGCCCTCGGT TTCCGTGATG ACTATGACCG TTTTACAGT CTCTCCGTG AAGGAAGTCC    540
GTGATGGCAG ACTCGGTAAC TATACCTTAG ATACATTGGA AGACCTCGAT GGCNACGATT    600
GAACTAAGTC C

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

TTGCTAAAGC	AGCCATGATG	ANGGCACTCC	ATAAGGATAA	GTACCACCAA	GCAGCAGCAG	60
ANGACCATAA	TCTCCTTTAT	GACTTGAACG	AGAACGTTCA	ATAATAACTT	TTTCTAGTAA	120
GGTTTGATTA	ATCACTTTCA	TCCTTTTTC	CTCTCACTTT	TATTATACAA	CAAAAAGGAG	180
ACGCAGACCT	CCTTTTGTA	TCTTATATCT	AAAATTTAAT	ATTCATTTCT	GCCATTTTAG	240
ATATAGCTAT	AGAAAATACA	CTCTATTAAT	CGAATGTTTC	TCTTATTTTC	TATCCAATGT	300
CCGAAGTGCT	GCTTGATAAG	TTTGCTCCAT	CAGCATGGTA	ATGGTCATAG	GACCGACACC	360
TCCAGGGACT	GGCGTGATAT	GGCTAGCAAG	TGGTGCAACT	GCCTCATAAT	CAACATCTCC	420
ACAGAGCTTC	CCATTTTCAT	CTCGGTCAT	CCCAACGTCA	ATGACAACCG	CACCTGGTTT	480
GACAAAGTCA	GCAGTCACAA	ACTTGGCGCG	GCCGATTGCG	ACTACAAGAA	TATCTGCTTT	540
AGCAGCCACC	TTGGCAAGAT	TATGAGTTCG	TGAGTGGGCC	AAGGTTACTG	TCGCATTTT	600
AGCCAAAAGA	AGCTGAGCCA	TAGGTTTTCC	AACGATATTT	GAACGACCGA	TTACGACCGC	660
ATTTTTACCT	TCCAAGTCAA	TCCCATATTC	ATGAAACATT	TCCATAATTC	CTGCAGGTGT	720
CGAGGGAATC	ATGACTGGAT	GTCCAGACCA	AAGACGTCCC	ATGTTTAGGG	GATGGAAACC	780
ATCCACATCC	TTTCTGGGT	CAATGGCTAA	TAAAACCGCC	TCTTCATCGA	TATGTTTGG	840
TAATGGCAAC	TGGACCAAAA	TCCCATGCCA	AGCTGGATCC	CTGATTATAT	TTAGCAATCA	900
GGTCTAACAA	TTCTCTTGA	GTTAATGGTC	TCTGGAATC	GCACTACTTC	GCTACGGGAA	960
CCAGCCGCAA	GAGCTGACCT	CTCCTTGTTG	CGAACGTAA	ACTTGGCTGG	CTGGATTATC	1020
CCCAACCAAA	ATCACTACCA	ACCAGGCACT	AGAG			1054

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTGAACTGGA	TTTTGCTACA	AGGTCTGATT	TGTCAAAGAG	ATGCGAGTTA	TGATATGAAG	60
CAGGATGATT	TGGATAAGGT	AGCAGATTAT	CTCTTCAAAA	CAGAAGAATG	GACCATGTAT	120
GAGTTGATTC	TTTTCGGTAA	CCTCTATAGT	TTCTACGATG	TAGACTATGT	CACTCGGATT	180
GGTAGAGAAG	TTATGGAGAG	GGAGGAATTT	TACCAAGAGA	TTAGTCGCCA	TAAGAGATTA	240
GTGTTGATTT	TGGCCCTCAA	TTGTTACCAG	CATTGTTTAT	AGCATTCTTC	TTTTTATAAT	300
GCCAACTATT	TTGAGGCTTA	TACAGAGAAG	ATTATTGACA	AAGGTATTAA	GCTTTATGAG	360
CGTAATGTTT	TCCATTATTT	AAAAGGTTTT	GCCTTATATC	AAAAAGGACA	GTGTAAAGAA	420
GGCTGTAAGC	AGATGCAAGA	GACCATGCAT	ATTTTTGATG	TGTTAGGTCT	TCCAGAGCAA	480

GTTAGCCTAT TATCAGGAAC ACTACGAAAA ATTTGTCAAA AGTTAATTTT CCCAAATAAG 540
 GGAAAAATA AAAAGCTCCT TTCGGTTTG ATACAATAGT TTCAAATTT GAGAGGAG 598

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTACTTCCCG GCCGAGTCGA TTCTCCGCCG ATATCGAGCA TACTGGCTCC TTCTGTTATC 60
 AATTTACGAG CTTGCTGGAG CGCCTGCTCA AGAGCAAAAA ATTGACCACC GTCCGAAAAG 120
 GAGTCTGGGG TTACATTGAT AATTCCGCAA ATAGCTGTCT TTGCATGAGT GGCTTTACTG 180
 GACATATCGG TCACTCCCTC AAGGCTATTC ATCATATTAT TTCTCTATTT TACCATAAAA 240
 AGAAAAAGAT GGACACGATT TCATTCATCT TTCTCCCAGT AGAAACAAGT AAGCAATTGT 300
 CAATAATCTT AAACAGAAAT CCCTAATGTC CGACTCATAA TCACCACAAG AGCCAACAAA 360
 CAGAAAGCAA TCCCATTAAC AATCATGTGA AGTAAGATCG ACATTTCCAA ACGTTGGGTC 420
 TTGTAGGCTG TCCAAGATAG AACTGTCGAC ATACCTCCAT AAATCAATAA AGAAGGTAAA 480
 TTACTTGGTT GATGTAATAA AGCAAACACA ATCGTACCGA CTACAAAT 528

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTATGAGAGA GAATGACCTT CTCTTGATTA CTGCGGACCA TGGAAATGAC CCAACGTATG 60
 CAGGAACGGA TCACACTCGG GAATATATTC CATTGTTGGC CTATAGCCCT GCCTTTAAAG 120
 GAAATGGTCT CATTCCAGTA GGACATTTTG CAGATATTTT AGCGACTGTT GCCGATAACT 180
 TTGGTGTGGA AACTGCTATG ATTGGGGAAA GTTTCCTTAGA TAAATTGGTA TAAGATGACC 240
 CGCTATGCTT TGCTGGTGAG AGGTATCAAT GTTGGTGGTA AGAATAAGGT CGTCATGGCG 300
 GAGCTTCGTC AAGAATTGAC AAACCTGGGA CTGGAAAAAG GTTGAGAGCT ACATCAATAG 360
 TGGCAATATT TTCCTTTACT TCGATAGATT CCAAAGCCCC AATTGGTTGA AAAAGCTAGA 420

GACTTTCTTT GCAGTCCATT ATCCATTTAT TCCAGAACTT TTTCCTTTAC TGAGTCTAGA 480
GGACTTTGAA GGGCGGAACT TGAAA 505

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CTATTTTCTC ATCTTTTTTA GACTGGTAAT GTATCCCCTA GAGTTTCATT GTTAAGACCT 60
GTCGTATTGA CAACAGTGGA TCCTGATTCC CCATTCCAAG AGTTTTGCCC GCATCATATN 120
GACGAAATCT TTTTCTGAGC CAGCAATTTT CTCAGCTAGG GCAATAGCGG CGCTGTTGGC 180
ACTAGATACC AGAGTTGCTT CAAGCAACTC TTCGACAGTA TAATTACGGG CCTCCATAGG 240
AATATTACTG GCTTCAGAAT TTGTCGTCAA TTGATAAGGA TAATCAGAAA TATCTACAGG 300
AGTGAGAGAG GTAATAC TTCGTTTTCCAA AGCTTCATAG ACCAGATAAA CAGTAATCAA 360
TTTTGTTATG GAAGCAATTT CGACAGGTGG CGTTGCATCC TTCTCATAGA GAATTTTACC 420
AGTATTTGCC TCAACAGCAA TCGCATGTTT AGCGGCAATG GTAAAATCTT GAGCAACAGC 480
AGTAGAAGCA CCCCCTAAAA GAGAGACAGT TAACAAAGTT AAAAAATATT TTTCATAGT 540
AGTCTTATTC TATCATAAAG AAAAAAATA TTCTTGCTTT AATAATTCAT CTGTTAAGCT 600
TTTTGAAAAT ATGGTAAAAT AAAGTGAGGG AGGTAAC TCA TGTTCGTAG AAATAAATTA 660
TTTTTTTGGG CCACAGAAAT TTTACTCTTA ACCATCATCT TTTACCTATG GAGACAGATG 720
GGGTCTTTGA TTAACCCTTT TGTTAGCGTG CTTAATACAA TTATGATTCC ATTTTATTA 780
GGGGGCTTTC TTTATTATTT GACAAACCCT ATTGTTACTT TCTTAAATAA AGTCTGTAAA 840
CTCAATCGTT TGCTTGGTAT TTTAATTACC TTGTGT 876

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTTGTCAAAT GCCATGGAAG GGGTTCTTTA CTTCTCAAA CCAGACTTTT CAAAAC TGAC 60

TAGCGCTGAT CTCCTCTATG CTCTGGGACA ATCTTCTTTT GCCCTCTCAC TAGGGGTAC	120
AGACATGTTG ACCTATGCTT CTTACTTGGA CAAGAAAACC AATCTAGTCC AGTCAGGAAT	180
CTCCATCGTA ACCATGAATA TCTCGATAGT CCATCATGGA AGGCTAGCC ATTTTCCCAG	240
CCATGTCAGC CTTCAATATC CACTCTGAAA GGGGACCCAG CCTGCTCTTT ATCGTCTTGC	300
CTCAACTCTT TGACAAGATG CCTTTTGGA CCATTGCTA CGTCCTCTC CTCTTTGCAA	360
CTGTCACTTC TTCTGTCGGT GATGCTGGAG ATCAATGTGG GCAATGTCAC CAACCAGGAT	420
AACAGCAAAC GTGCCAAATG GAGTGTATT TTAGGAATTT TGACCTTGT CTTTGGCATT	480
CCTTCAGCCC TATCTTACGG TGTCATGGCG GATGTTTACA T	521

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCAGACAA TAACTTGGTT AGCTTAACGG CTCTTGAGGA TTCATCCAAG GATGTAACCT	60
TTACCAAGTTC GGCTTTCAAT CTAAAAGAAG GGCGACACCT TCAAAAAGGG GATTCCAAGA	120
AAATCCTTAT CCACGAAGAA TTGGCTAAGA AGAACGGTCT TTTACTTCAT GACAAGATTG	180
GCTTGGATGC TGGTCAGTCT GAATCTGGAA AAGGACAAAC AGTAGAGTTT GAGATTATCG	240
GCATCTTTCC TGGTAAAAA CAAGAGAAAT TCACAGGCTT GTCTTCTGAC TTCAGTGAAA	300
ATCAAGTCTT TACAGATTAT GAAAGTAGCC AAACCCTTTT GGGCAATAGT GAAGCTCAAG	360
TCAGTGCAGC ACGCTTCTAT GTTAGAAAAT CCTAAGGAAA TGGACGGACT CATGAAGCAG	420
GTAGAAAAC TGGCCTTGA AAATCAAGGC TACCAAGTCG AAAAGGAAAA CAAGGCTTTT	480
GAACAAATCA AAGACTCAGT TGCAACTTTC CAAACCTTCC TGACCATCTT CCTTTATGGA	540
TGTTGATAGC AGA	553

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTATGGATGC	GGAAGTTTCT	AAGAACCTTC	GCTTGATCCT	TGAGCGTAAA	GGAATGACCA	60
TCTTGACTGG	TACTAAACTG	CAAGAAATCA	TTGAGGAAAA	TGGTCAACTT	CGTATCAAGG	120
TTGAAGGAAA	AGACAATATC	ATCGCAAGCA	AAGCTCTTCT	TTCAATTGGT	CGTATGCCAG	180
ACCTTGAAGG	TATTGGAGAG	GTTGAGTTTG	AATTGGATCG	TGTTGTATC	AAGGTCAATG	240
AATACATGGA	AACTTCAGTT	CCACGCATTT	ATGCCACCAG	GTGACATCAA	CGGTACTAAG	300
ATGTTGGCTC	ACGCAGCTTT	CCGCATGGGT	GAAGTTTCCG	CTGAAAATGC	CCTTAAAGGA	360
AATCATGCAG	TTGCCAAATT	GAATTTGACT	CCTGCAGCCA	TCTACACTCT	CCCTGAAGTA	420
GCAGCAGTAG	GTTTGACAGA	AGAACAAGCC	CGTGAGAAAT	ACGATGTTGC	CATCGGTAAG	480
TTTAACCTTG	CTGCTAACGG	TCGTGCTATT	GCATCTGACG	CAG		523

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CTGCAGGTGG	AATTATGAAT	GTCGGATATG	AAAAAGCATT	CTTGATGCAG	ACATCGTTAA	60
ATTTGCCAAC	TTCTGAAATT	ATCTCGACAT	ATGTCTATAA	AGTTGGTCTT	GTATCAGGAG	120
ACTATTCTTA	CTCAACAGCG	GTTGGTTTGT	TTAATGCAGT	GATTAACGTA	GTATTGCTTG	180
TTGCAGTTAA	CCAAATCGTT	AAACGCATGA	ATAATGGTGA	AGGAATTTAA	GGAGGAAAGT	240
ATGAAAAATT	CGATTATGGA	TACAAAATTT	GATAGACGTA	TCTTACTCTT	AAATAAAATC	300
ATTATTGTCT	TTATCGTTTT	GATGACTTTG	CTTCCTTTAC	TTTATATCGT	CGTAGCATCC	360
TTTATGGATC	CTAAGGTTCT	GGTTAGTAGA	GGGATTAGCT	TTAATCCAGC	CGATTGGACT	420
GTAGAAGGTT	ACCAGCGTGT	TATTCAGTGA	CCAATCTATT	CTAAGAAGTT	TTATCAATTC	480
CCTACTATAC	TCTTTTGGAT	TTGCAGCT				508

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTAAAAAGAA	CCAGATGGAT	CTTGTGATGA	ATTTACATCA	TTTTGATTTA	CCAGTGGAAC	60
TTCTTCAAAA	ATACGGTGGT	TGGGAAAGCA	AACATGTAGT	GGAGTTATTC	GTGAAGTTTG	120
CCAAGACTGC	TTTCAACATG	CTTTGGAGAT	AAGGTTTCATT	ACTGGACAAC	TTTCAATGAG	180
CCAATGGTCA	TTCCAGAAGC	AGGATACTTA	TATGCTTTCC	ATTATCCAAA	TCTAAAAGGA	240
AAGGGAAAAG	AGGCCGTACA	AGTCATCTAT	AATCTAAACC	TTGCTAGTGC	AAAAGTGATT	300
CAACTATATC	GCTCATTAGG	ACTTGATGGA	AAGATTGGGA	TTATTTTAAA	CTTGACACCT	360
GCTTATCCAA	GAAGTAATTC	TCCAGAAGAC	TTAGAAGCAA	GTCGATTTAC	AGATGACTTC	420
TTTAACAAAG	TCTTCCTTGA	ATCCAGCTGT	TAAAGGAACT	TTCCAGAAA	AGATTGGTAA	480
AAACAGCTAG	AGAGAGATGG	CGTGTATATG	AGTCATACCG	AAAAAGAG		528

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACTCTTATTG	GTGAGGTATC	GCAACTTCTG	TTTCTGCCTT	CCTTGGTGGA	CCAGCCAATA	60
CAACTTACGG	AGAAAATACA	GGGGTTATCG	GTATGACTCG	TATCGCTTCT	GTCTCAGTTA	120
TCCGTAACGC	TGCCTTCATC	GCGATTGCCC	TCAGCTTCCT	TGGTAAATTC	ACTGCCTTGA	180
TTTCAACTAT	TCCAAACGCT	GTAATTGGTG	GTATGTCAAT	CCTTCTCTAT	GGGGTTATCG	240
CCAGCAATGG	TTTGAAAGTC	TTGATTAAAG	AACGTGTGGA	TTTCGCTCAA	ATGCGAAACC	300
TCATCATCGC	AAGTGCTATG	TTGGTTCTTG	GACTTGGGAG	GAGCTATCCT	TAAACTTGGT	360
CCAGTTACAC	TTTCAGGTAC	TGCCCTTTCA	GCCATGACAG	GAATCATCTT	GAACTTGATC	420
TTGCCATACG	AAAATAAAGA	CTAAGAGTCT	AAATACACCT	AATCCACTCA	GACAGCTGAG	480
TGGATTTTTT	GTATACCATA	ATAAAAGTGT	CTTAACAAAA	TTATTAAAAT	CAAAAAACGT	540
ATAATATCAG	ATATTCTAAA	ACCTTGATAC	TGTACGTTTT	ATCATAGAAA	TTTTTACTTT	600
ATTTTCTCAT	CAAATGAGAT	TTGCATCAAT	CTCTTGCTTT	ACTTGCGTTT	CTTCTTCGCT	660
TTCTTCATTT	TGTTAGCCAT	ACGTTTCATG	GACTGTTTCA	TGGCAAATTC	ACCAATTTTA	720
CCTTTCAAAC	CGCCACCAAA	CATCTGGCTC	ATATCTGGCA	TTCTGCTCC	TCCGAGAG	778

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

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GGGAGTTGGT TGCTATTNGT GAGGGAAAAG GTTTGAACCT TGAAATCGAA GTGGATGGTG      60
GGATTGATGA CCAAACCTATT GCTCAAGCCA AAGAAGCTGG TCGACTGTT TTTGTAGCAG      120
GTCCTATGT CTTTAAGGGA GAAGTCAATG AGCGAGTACA AACTCTCAGA AAACAACCTGG      180
ACTAGGGTTG CAGTTTTTGC AGGCGGAAAC CGCGGTCATT ATCGGACAGA TTTTGATGCT      240
TTTGTTGGGG TGGATCGAGG CTCGCTCTGG GTCTTGGAAG AAGACTTACC TCTTGCTCTA      300
GCAGTCGGAG ATTTTGATTC TGTGACGGAA GAAGAGCGAC AGGTGATTCA AAAACGTGCC      360
CAGTATTTTG TCCAAGCCCG GCCAGAAAAA GATGATACTG ATTTGGAATT GGCTCTCTTA      420
ACCATCTTTG AACAAAATCC TCAGGCTGAG GTCACTATTT TCGGTGCCTT GGGTGGCCGT      480
ATTGACCATA TGTGCGCCAA GTTCTTTCT ACCTAGCAAT CCCTAAGTTG GCACCCTATA      540
TGCCTTCNAA TAGAAATTGA GGAATGGGCA AATTTGATTG CCTATTGTTT CAGAAGGGAA      600
CAGTCAGATT CGAATCCCTG CA                                     622

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(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

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CTATTATCAG CACTTTTATA CCTATTACCA AAAAAATCCT CAAAATGATT GGCAAAAGGC      60
TTTATCCACC AGCCATTTAT CAGCAATATT TACTTGAAAA ATATGGTAGA AATAGAAAGG      120
ATGGAGGAAT CTAATGGTAT TACAAAGAAA TGAATAAAAT GAAAAAGATA CATGGGATCT      180
ATCAACGATC TACCCAACCTG ACCAGGCTTG GGAAGAAGCC TTAAAAGATT TAACAGAACA      240
ATTGGAGACA GTAGCCCAGT ATGAAGGCCA TCTCTTGGAT AGTGCGGATA ACCTACTAGT      300
AAATCACTGA ATTTTCTCTT GAAATGGAAC GCCAGATGGA GAAGCTTTAC GTTTATGCTC      360
ATATGAAGAA TGACCAGGAT ACACGTGTAA GCTAAGTATC AAGAGTACTA TGCCAAGGCC      420
ATGACACTCC TACAGCCAGT TAGACCAAGC CTTTTCATTC TATGATCCTG AATTTATGGA      480
TATTAGCGAA AAGCAGT                                     497

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(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGTTATGGA GTTGAAAGAA GAATACCACC CAGACGGTAA AGGTTTGTGA ATGATCTGTA	60
TCGGTGGGAT GGGAGCTGAT TTC'TTTAAGG CTCGCGGTAT TCAACCACTT TATGAATTAC	120
GTGGCTTGTC AGACCAACCT AGCTTTGATC AAGTTCGTAA GATTATTTC AAAAACTGTTG	180
AAATGTACCA AAATGAACTC TTTGATGAGC TTTATGTTTG CTACAACCAC CATGTCAATA	240
CGCTAACCAG TCNAATGCGT GTGGAACAAA TGCTTCCGAT TGTTGACTTG GATCCAAATG	300
AAGCGGATGA AGANTACAGC TTGACTTTTG AAATTGGGAA ACCAGCCGAG AAGAAATTCT	360
GGAGCAGTTG TTGCCTCAGT TTGCAGAAAG TATGATTTAC GGTGCCATTA TCGATGCCAA	420
GACAGCTGAG AATGCTGCGG GTATGACAGC CATGCAAACA GCGACAGATA ATGCTAAGAA	480
AGTCATCAAT GATTTGACAA TTCAGTATAA CCGTGCCAG ACAGGCGGAT ATTACACAAG	540
AAATTACCGA AATCGTAGCA GTGCCTAATG CCTTAGAATA GCTCTAGTCC CAGCTCTCCT	600
CACTC	605

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CTACACTTGA GGGAAGTTTG AAAATTCCAT TTTTCTTAAA GGGAATTGTG AAACGCTATG	60
TATTTTCTTT TTACAACCGG ATGGAGCACT TGGTTGTGGT CAATCCTATG TTTATTGAGG	120
ATTTGGTAGC AGCTGGTATT CCACGTGAAA AAGTGACCTA TATTCCTAAC TTTGTCAACA	180
AGGGAAAAAT GGCATCCTCT ACCACAAGAA GAGGTAGTCA GACTGCGCAC AGATCTTGGT	240
CTTAGTGACA ATCAGTTTAT CGTAGTAGGT GCTGGGCAAG TTCAGAAACG TAAAGGGATT	300
GATGACTTTA TCCGTCTGGC TGAGGAATTG CCTCAGATTA CCTTTATCTG GGCTGGTGGC	360
TTCTCTTTTG GTGGTATGAC AGATGGTTAT GAACACTATA AGAAAATTAT GGAAAATCCC	420
CCTAAAAATT TGATTTTTC AGGCATTGTA TCGCCAGAGC GGATGCGCGA AATTGTATGC	480
TCTAACGGAT CTTTTC'TTGT TGCCTAATTA CAATGAG	517

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTGCGCTC CATATCCNAA ACTTGCCCTG CCACCATACC CAGACTACCT GAAGCAAGGG	60
ATAAGTTGGC AATCGAGCCC ACCTNGATCT GACTTGGCGA ATCTGCCTGC GCAATCAAGG	120
CATATGGGTC TAAGAATAAG GATCTCCAGC CAAAATGGCC ATAGCTTCAC CGAATTTCTN	180
GTGATTGGTT AACCGCCCTC TTCGATAATC GTCATCATCC ATAGCAGGAA GGTCATCGTG	240
AATCAAGCTC CCTGTATGAA TCATCTCCAA GGCAGTAGCT ACCTGCGCGN GAGCAGGTTT	300
GATGGTAACC TGCAAGGCTT CCAGAACTTC TAACAAGAGA AAAGGCCGAA TACGCTTGCC	360
ACCAGCATGA ATAGAATAGA GAACAGACTC CCGTAAACTA GAGGCAAAC TCTGGTCTCC	420
ATAAAATCTT CCAAAGCCGA CTCGACAAGA GCTAATTTT CTTGCTTTT CATTCAAAAT	480
CACTTTCTGT TCCGTCCTCT TGCATGACCT TGACCAAGGT CTTTTCAGCC TTGTCCAGCG	540
TAGCTTGGAG CTCTTTTGAC AAGACCATGC CCTTTTGAAA GGCAGTAATC GCATCTTCCA	600
GAGCAATTTT ACCATTTTCC AAACCTTTGGA CAATGGTTTC CAGTTCTGCT AGATTTTCCT	660
CAAATTTCTT TTGTTTGTAC ATCTTTAACC TCTAATTCTA CTTGACCATC TCGCATCAAA	720
AGCGTACTT GGTCTTTTCT CTTCAAAC TCAACCGAAT CTACAACGGA TCTTCTTTT	780
TGACAATAGC ATAACCAC	798

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CCATGTTTGC GGCAGTGACA GCAGGTTATC AGGCTGCCCT AATGGTACCA ACAGAAATCC	60
TCGCAGAGCA AACTTTGAG AGTTTACAGA ACCTTTTCC CAATTTGAAA CTGGCTCTCT	120
TGACAGGTTT CTTGAAAGCT GCAGAAAAGA GAGAAGTCTT GGAGACCATT GCCAAGGGTG	180
AGGCTGATTT GATTATAGGA ACTCACGCTC TGATACAAGA TGGGGTGGAG TATGCTCGTC	240
TTGGTTTGAT TATTATCGAT GAGCAGCACC GTTTTGGTGT AGGGCAAAGG CGTATTTTAC	300
GGGAAAAGG CGACAATCCA GATGTCCTCA TGATGACGGC GACTCCATT CCACGGACGC	360
TTGCCATCAC AGCCTTTGGA GATATGGATG TTTCCATTAT CGACCAGATG CCAGCAGGTC	420
GGAAGCCCTA TTGTGACGCG CTGGATCAAA CATGAGCAAC TACCTCAGGT CTTGACTTGG	480
TTAGAGGGGG AAATTCAAAA AGGTTCCCAA GTCTATGTCA TCTCTCCTT GATTGAAGAA	540

TCAGAAG

547

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CTCTTTTAAC CGTTTTAGCG GTGACACCGA GGTATTTTTT CAGGACCCAA GACTTGTCGG	60
GCAACCGAAA CTGGGAGTTC GTCATCTCCA ATATGCAGAC CAGCAGCATC AACCGCAAGA	120
CAAACATCCA ACCGATCATC GATTATCAAG GGGACCTGAT AGGCATCTGT TATTTCTCTG	180
ACTTGTTTTG CCAGTTGATA ATATTGATTG GTTGTGAGAT TTTTTTCTCG CAATTGGACT	240
ATGGTAACCC CTGAACGGCA GGCCGTCTCA ACTTTTGCAA GAAAGCTTTC CACGGAATCT	300
TGATAGCGAT TGGTTACCAG ATATAGTCTA AGCGCTTCTC TATTCATAAA CCTCTCCTTT	360
GATGGTATCT AGCCAATTTT CATCTCTTCT TAGGAGCGAA AGCTGATTGA GTACTTGGTA	420
ACGAAATTCT TCCAATCCCA TTCCTTGAAC AACTATTTTC TCAGCCAGCG ATATTGAGAT	480
AAGAGACTGC TAAGCAAGAA CTTCAAAACC AGTCTTTCCT TGGCTGAGAA AAACAG	536

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CTGGAGTGAC GATTGAGAAA ATCTTTGCCC TAGAAAATTA TCGAAATCAG TTAGCTGCTT	60
TTCCGCAAAC TGTCTGGATT TCAGAGGATA TTTTGCTAGA TTTGGCGGAT TCTCAGACTC	120
CACAGGGAAT TGTTGCCGTG GTTCAAAAAG AAGAAGTAGG ACAAGCTGAT TTGAGTCAGG	180
GCAAGTCTT GTTTTTGGAA GATGTGCAAG ATCCTGGTAA TGTAGGAAC ATCATTGCAA	240
CTGCGGATGC AGCAGGTTTT ACAGGAGTGA TTGTTTCAGA TAAGTCGGCA GACATCTACA	300
GTCTTCAAAA CCCTACGTC CATGCAAGGT AGTCATTTCC ATCTGCCCCAT TTACCGGATG	360
ACTAGTCAAG CGCTTCTTGA CGAAACTAAA AAGGTAGCTA TCCCAGTGCT AGCAACAACC	420
CAATCTAAAG ATTCTGTTGA TTACAGAGAA CTGCCTTCTA TAGAAAATTT TGTACTAGTT	480

ATGGGAAATG AGGGTCAAGG AATTAGTCCC CTTATGGCTG AAAGTGCAGA CCAGTTGGTC	540
CATATTAGCA TGAAGGGGCA GGCCGAGAGT TTGAATGTTG CGGTTGCAGC CGGTATTTTA	600
ATCTTCCATT TAAGCTAATT TTAACTTTTT TTGTTATAAT CAAGGAAAGA TGTTACAGA	660
AAAGGAGAAA TGGATGAATC ACACTATTAT ACATGACCGT GCAGGTCTCA ATCAATTTTA	720
CGCTAAGGTT TATGCCTTTG TTGGTCTGGG AATCGGACTA TCTGCTTTGG TATCAGGCCT	780
TATGTTGACG GTCTTTCAGT CTCAGTTGGT TTACTTTTTG ATGCAGGGGC GTCTCTGGTT	840
GACCATTGCT ACTT	854

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA GAAGAAGCCT	60
CTCGCTGGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT TTTTATTTGC TGGTCAAGGT	120
GCCAGTATC TACGGATGGG ACGGGATTTT TATGATCAGT ATCCGATTGT CAAAGAAACG	180
ATTGATCGAG CGAGTCAGGT GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA	240
GACAAACTCA ATCAGACCCG CTATACGCAA CCAGCCATTC TAGCGACTTC GGTGCTATC	300
TACCGTTTAT TGCAAGAAAA GGGCTATCAC CCTGATATGG TTGCTGGTTT GTCTCTGGGA	360
GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTTTG AAGATGCCGT TGCCTTGGTA	420
GCTAAGCGTG GAGCCTATAT GGAAGAAGCG GCTCCTGCTG ACTCTGGCAA GATGGTAGCA	480
GTTCTCCATA CCCCCTAGAG TCCTTGAGAA GCCTGTCCAA AGCTCTGACT TGAGTGGTAC	540
TCCAGCCACT ATACACACTG CACAATCTCA TTGCTGGAAA ATTGTTGCAG TGATCAACGG	600
TGACTTTGCA GAGCAGTGCC AACCTATCC CCTAGT	636

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTCTAAAACG AATTCTCTAC AAGCACCGCA AGGGCATGGC TGAACCTCCA CCATAAGGTG	60
GTTTGTCTCG AAAGGCTAAT ACTTCNTTAA CCTTAGTTTG TCCTGAAAAT TGGTACATAT	120
TGAAGAGGGC CGCCCGTCT GCGCAGAGAT GGAACACACC ACAGGTCCC TCCATACAGA	180
ATCCTGTAAA TATTTGTCCA TCTCCTGCTT CTA CTG CAGC TACAACATGA TTGGCATAAA	240
CAAAGTCTGA TACTTCATGT GGATTGTATA GTTTCTGTGC TTCTTCCTAC ATCTTTTCCC	300
AGATGTCCAT TATTGTATCC TCTATATTTA GAGATTTCTT TTAGAATGTT TTCGATATGC	360
TGAATTGATT TTTCACGTCC AAGCAAGAAA ATTGTATCTG GTAATTCTGG CCCATGCATT	420
TCGCCTGAAA CTGCGATACG AATAGGCATG AAAAGATTTT TCCCTTTAAT ACCTGTTTCT	480
TTTTGGACTG CTTTAATTTG CGGGAAGATA TTTTCTGTCA CAAATTCATC ATCTGTCATC	540
CGCTTCAATT TTGCTTTGA ATGCTTCAAG AACTGTTGGA ACTGTTTCAC CCGTCATGAC	600
TTCGCGCTCT GCTTCTGTCA ATTCCTGGGA AATCTGAGAA GAAAGATCTG TCCATGGGAT	660
ATCTCATCTA CTGATTCATT GTGGTTTATA GAG	693

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CTGACAAAGG AGACGGGTAT GGAACAAACA TTCTTTATCA TCAAACCAGA TGGTGTA AAA	60
AGAGGGCTAG TGGGTGAAGT GTTAAAGCGC ATCGAACAAC GTGGATTTAC AATCGAAAA	120
TTGGAGTTTC GTTCACAGGT TTTCAGAAGA GTAGATTGAC CAGCACTATC AGGACCTGGT	180
TGGTCAGAGT TTTTACCCAC CGATTCGTGA ATTCATGACT TCAGGTCCAG TTCTTGTGGG	240
TGTCATTTCT GGTCCCAAAG TAATCGAAAC TTGGCGGACC ATGATGGGTG CAACTCGTCC	300
AGAAGAAGCT TTACCAGGCA CTATTCGAGG TGATTTTGCA AAAGCTGCTG GAGAAAATGA	360
GATTATCCAA AATGTTGTAC ATGGTTCAGA TTCCGAGAAG AATCAGCTAA GCCGAGAAAT	420
TGCTCCTTTG GTTTTAAGAG TGGATTGGCT CAATCAATTG GATAAAAGCT CATTTGAATA	480
GAAAGTATAG TCAATTAGTT TAAGACATGA CGCATGATAT CAAACTTTTT AGTTTTTGAT	540
ATGGTGCGTT TTT	553

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

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CTAGAGATTT NCGAAGAGTA TTATTGTACT TTAAAGGTCT TGAGATAATT GTCTTTNCCT      60
ACTTGACCTT CGAAGGTTTT ACCATTTTCA AGGTAAGGAA GGTCATCGGA TACTGAAGCC      120
TTGACCTTGT ATATCTTGCC ATCAACTTTA AAGAAGTAGA CAGTGTCTCC CTTGATAACA      180
GCTGATTTGA GGTCTGCTAC TACTCCCTTG ATGCTTTCTG TCGTTGCATT GTCAATTTCA      240
AGGTCGTTTT TATTGGCATA CTTGCTGAGC ATCTCTTCCA CTGTAGTAGC AACGATAACA      300
TTTTGGTACT CGACTGCGTC TACCAGGGCG TACTCTTTGA CCAAGCCAGC ATTGTCCTTT      360
AAGCCCATGA TGTAAGAGAG CTTGTCATTG AGGTTGATAA AGATTGGGGA AAGGTTGCTT      420
TGTAGGATTT CTCCTGAACA GCACCTTCTG CTGATTCACG GGCTGATTCT TCTGTCGCAG      480
AAGCCAAG                                         488

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(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

TACAGCTATC GGGTCCGTCT GGTAGTTGGT CCTCAGAACC TTCACTGCCA CTCTTTCCCC      60
ATCTAAGATT AAGTCTTTGG CTAGGTAGAC ATCCGCCATG CCTCCTCGAC CAATCTGTTT      120
GACAATCCGA TAGCGTCCGG CAAAAATCTT GCCGATTGG ATCATTCTTC ATCCTCCTCG      180
TTCATAGAAA CAAGGGCAAC CGTAATGTTG TCTAAACCTC CTGCATTGTT AGCAAAACGA      240
ACAAGTGTCT CCGTTTTATC TGCTAAAGGA ATATCACTGG TTACAATATC ACGAATCTCA      300
CTGCCTGAAA TCATGTTGGT CAAGCCGTCA CTATTGAGCA AGAGATAGTC ACCTGACTCA      360
AGGATAACTG TCCCAAAATC AGGCTGAATT TCATCTTTTT GCCCAATAGA CTGGGTGATA      420
ATATTTTTTT GTGGATGACT TCTGCCTCTT CTGGTGTCAT TTGACCAGCC TTGAGCAATT      480
CATTAACCAA AGAATGATCG CTCGTCAACT GATGGTATCT TCTCCACGAA TCAAGCCGAT      540
ACG                                         543

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(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAAATTA AATAGTAAAA    60
AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACAA CTAATAGGCT    120
AGAATGGACA TAGTAAGATN TAGTAGATGA GTCATTCTAC TCAAATCCAC GTTAGAAAAG    180
ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC    240
GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGA AGCCAACCGC    300
CTGTCCTCCA TGATTCTATA TGGCCCTCCT GGAATCGGCA AAACCAGTAT TGCCTCTGCC    360
ATCGCTGGAA CGACCAAGTA TGCCTTTCGA ACTTTC AATG CGACAGTTGA TAGTTAAAAA    420
GCGACTGCAA GAAATCTCGG AAGAAGCTAA ATTNCTGGT GGTCTCGTCC TATTGCTAGA    480
CGANATTCAT CGACTAGATA GACC                                           504

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(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

CTAATAGAGG CGAAAAAATT TCAGGTCCTC CTTTGCTAGA TGATAATGAG GAAACTAAGA    60
TTTTACCAAC CTCTTCTTCC CGTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC    120
AGGAAACCTT GAAGATTTCAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA    180
CCAAGAGAAA TGTCTTCAAT TCTAAGTTGA ATAAAATCTT ATTTGCGGTC ATCTTCTCT    240
TGATTTTGCT TGTTTTAGCA ATGAAACTTT TGTAATAGAA AAGGAATTGA AATGAAAATA    300
GGAATTATTG CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATTT AGATAATGCC    360
CAGGAGCAAG TTGTTTGGG GAATACCTAT CATAAGGAA ACCATTGCTT CTCATGAAAG    420
TCGTTCTTGT TAAAAAGTGG AATTGGTAAG GTCATGTCTG CTATGAATTG TGTGGCGAAT    480
TTTGGCTGAT CATTTCCAGG TTGGATGCCC TTATTAATAC GGGTTCAG                    528

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(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTAATAAGAC	TGAAAAGAAG	TCCAGCCAGA	TGTCCTTAAA	AATACAGAAA	AAACATTAAA	60
ACCAAAGGAA	ATCAAATTTA	ATTCTTGGGA	AGAATTGTTA	AAATGGGAAC	CAGGTGCTCG	120
TGAAGATGAT	GCTATTAACC	GCGGATCTGT	TGTCCTCGCT	TCACGTCGGA	CGGTCATTTA	180
GTCAATGAAA	AAGCTAGCAA	GGAAGCAAAA	GTTCAAGCCT	TATCAAACAC	CAATTCTAAA	240
GCAAAAGACC	ATGCTTCTGT	TGGTGGAGAA	GAGTTCAAGG	CCTATGCTTT	TGACTATTGG	300
CAATATCTAG	ATTCAATGGT	CTTCTGGGAA	GGTCTCGTAC	CAACTCCTGA	CGTTATTGAT	360
GCAGGTCACG	TAACGGGGTT	CCTGTATACG	GTACACTCTT	CTTCAACTGG	TCTAATAGTA	420
TTGCAGATCA	AGAAAGATTT	GCTGAAGCTT	TGAAGCAAGA	CGCAGATGGT	AG	472

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CTTTTAAATA	AGAAGAATCA	CACTCATTCG	TAAATGTGAT	ATAATATTGT	TCTCAGTCTC	60
AGCAGTGCGT	TGTGAAAAAG	CCATACTAAT	CCCTGATTTT	TCCGCATATT	CCATCACCTC	120
AAGTGTTTTA	CTCACTGAGC	CAACTTGATT	AGGCTTTATT	ACAATACCAT	CAGCACAATC	180
TTTAAACTGT	GAAATTCCTT	CTAAGTTTGT	TGCGTAAAAA	TCATCACCAA	AAACTTGTA	240
CTTTAGAGGT	TTTATCAATT	GAAATTTTCT	CCAACATATC	AAATCTTCAT	CGGAAAATGG	300
ATCTTCAAGA	TAAACCAATG	GATACTTAAC	TCCCAATCA	CAATAAGTAT	CCATAATTTT	360
TGTGACTGTC	TGTTGCTGAC	TAACACACCA	TGGTACTTTA	TATATGCCAA	GTGAAGAATC	420
GTAACGATCT	GTCATTGCTA	AATCTAAACC	GATATCATAT	CTATTTTGT	ATAATTTTAA	480
TGTCTCTAAT	AACGAATCCA	AAATAATATA	AAAATCATCC	GTGTTAATTA	TTAATGCACC	540
TTGATAGAAA	TAGATGTTGT	AGAAACCTGG	GTTTAACTT	TATCATAACT	CATTTTATG	600
TTAGA						605

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTGAAGAAAA TCAGTAAACA AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT	60
TTTGGACAGG AAAAAGACGG TAGTTTTCTT GCCCAGCGTT ACCAATTTTA CCTCGCCCAG	120
CAGGGACAAA CACTATCGGG CGCTCATGAT CTCTTGGACA GCCTCATTGA GCGTGATTAT	180
AAC TTGTATG CTGCGACAAA TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT	240
GGTCTAGCAC CTTATTTCAA TCAAGTCTTT ATCTCAGAAC AGTTGCAAAC TCAAAAGCCG	300
GATGCTCTTT TTTATGAAAA GATTGGCCAG CAAATTGCTG GATTTAGTAA AGAAAAGACC	360
TGATGATTGG AGATTCTCTA ACCGCCGACA TTCAAGGTGG CAATAATGCG GGGATTGACA	420
CTATCTGGTA TAATCCTCAT CACCTCGAAA ATCACACACA AGCCCAGCCG ACTTACGAAG	480
TCTATTCTTA CCAAGACTTG CTGGATTGTT TAGATAAAAA TATTCTTGAA AGATCACGTT	540
TTAAGGAGAT AG	552

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CTTTGTCTGT ATCTGCCTTT TTATGCTATA CTTAAGGTAT GCATAGAAAA ACAGTGATTG	60
ATTNTAGGAC TTTAGGGGAG AGATATACCT TTACCCANCC TATTAAAGAG TTGAAAACGA	120
GAAATGTAGC AGAAGTGGCA GATTTGCTGG CACNAGTGA AAGCTACCAA GAGCAAGATT	180
ATTATGTGGT GGGGTATGTC AGCTACGAGG CTGCACCTGC TTTTGAGGAG AAATTAGCAG	240
TTCACAAGGT TCCTCTACTG GCGAGTACT TGCTTTACTT TACTGTTTAC GATAGGGTGG	300
AGACCTCCCC TATTCCTCTG ACTTATGAGG ATATTGATTT GCCCTCAAAT TGGCAGGGAA	360
NTAACGTCTG CACAGAACTA TGANAAGGCC ATTGCCCAGA TACAC	405

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTCAAAAACA	GCTTCTAACA	GCTTGAACAA	GGGGGCTAAA	ATTGATTCTT	TGATGTAGGG	60
TTTGAAGTAA	GATAATAGGT	GTTTCATAAA	TCCCTTCTAT	TCATATTCTA	GAAATGAAGA	120
AAGTGGGAAG	CCCCACTCTC	TGTTTTATTT	GTTTAAGTAA	GGCAATAGAT	AGCCATATCC	180
TGCTTTTTC	ATCTCATCCT	TGGCCACAAA	GCGTAAAGAA	GCAGAATTGA	TACAGTAACG	240
GAGGCCGCCT	AACTCCCGCG	GTCCATCTGT	GAAAACATGA	CCCAAGTGAG	CACTGCCTGA	300
ACGAGAACGA	ACTTCAATTC	GCTCCATTCC	ATGGCTCAGA	TCCTTGTAAT	AATGAATCAA	360
CTCTTTGGAA	ATCGGACGGC	TTAAACTTG	GCCAACCCAC	AACCTGAAGC	AACTTATCC	420
TTGGCAAAA	AGAGTTGGCT	CACCTGTTCT	TAATATCTAC	ATAAATCCCC	TCCTTCCAAA	480
GGTTTTGGTC	CATAGGCATT	GGTAAATGGA	CCTCCTGTTA	CCAG		524

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTTCATCTGG	TGGTTCTCCA	GTTGTAAGTA	ACGTAGTACC	ATTCTCAAAA	CCATACTCAC	60
AAGTTGGTAT	TAAGGGGGAA	CCATATATCT	TTAAAGGAAT	GAAATTGCAA	AAAGATATTG	120
TTACAACAAA	AGAATATAAC	GAGGTTTTAA	AAAATGGCAA	AAAGAAAAAT	TGGAATCCAA	180
TAGCAAATAC	CAAAAAGAAC	TAGAAAAATA	CATTAAATAA	GGAATGGTAT	TGATCTTGAT	240
AAAATTTTTA	AAATACTGTC	ATTTTGAATA	TAAAGGAGTT	TGATATGGAG	TGGATTAGAT	300
TAATAGGAAT	AGCAATCATT	GTTGTGGGTT	TTATTTTAAA	ATTTGATACA	ATTGCAACAG	360
TAGTCTTAGC	TGGTTTGGTT	ACAGCTTTAG	TTTCAGGTGT	TTCTCTCGTT	GAATTTTGG	420
AGATTTTGGG	AAAAGAATTT	AGCAATCAGC	GAGTGCTCAC	GATTTTATG	GTTACCTTGC	480
CTCTTGTTGG	GCTGTCAGAA	ACCTTTGGAC	TCAACAACGA	TCAATCGATT	TGATTCGAAA	540
GATTAAAGGT	CTGACAGTTG	GAAACTTCTA	TACAGTTTAT	TCTTTATCGA	GAG	593

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CCTGCTCCTT ATCTTTGCAG TAATTGGCGT TTTAGTGGCC TTGATAGCTC AATTTTACTC	60
AGCAAAGGCA GCAGTAGGTT TTGCTAAGGA ATTGACAAAC GATCTTTATC GTCATATTCT	120
TTCCCTTGCCC AAGGACAGCA GAGACCGTCT GACAACCTCT AGTTTGGTTA CTCGCTTGAC	180
TTCGGATACC TACCAGATTC AGACTGGTAT CAATCAATTC CTGCGTCTCT TTTTACGAGC	240
GCCCATTATC GTTTTTGGTG CCATTTTAT GGCTTATCGA ATCTCAGCTG AGTTGACTTT	300
CTGGTTCTTA GTCATGGTTG CCATTTTGAC CATTGTCATT GTTAGGGTTA TCTCGATTGG	360
TCAATCCTCT CTACAGTAGT CTCAGAAAGA AAACCGAACC ACTGGGTTCA NGAAACCCCC	420
CNCCATTGCA AGGATGCCGG GTTATTCCGT GCCTTT	456

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTGACAGT TGAATCGTTC AGATATTGAT TTTGAAAACA GAGAGTGTGT TGTCTTTGGT	60
AAAGGAAAGA AGGAGAGACC AGTATATTTT GACGCTCGGA CGAAAATTCA TTAAAGAAAT	120
TATCTTAACG ACAGAAAAAG ATAGTCACCC TGCTCTTTT GTAACGCTAG TTGGAAAAGC	180
CCAGAGACTT GGAATTGCTG GTGTAGAGAT TCGCTTAAGA AAGTTAGGAG ACAAACCTCGG	240
CATACAAAAG GTTCACCCAC ATAAGTTCAG AAGAACTTTA GCGACTAAGG CAATTGATAA	300
AGGTATGCCT ATCGAACAAG TCCAAAAACT GCTAGGTCAT AGCAAGATTG ACACAACCCCT	360
GGCCTATGCC ATGGTCAATC AAAATAATGT CAAGCATTC CACCAAAAAT TCATCTCTTA	420
AAAGCAAATC CCGATATTCC GAAGAGGTGG TTGCATGAAG AAAGTGAAAT TAGGTGAAGT	480
GGCTACTTTT ATCAATGGCT ATGCTTTTAA ACCTCAAGAT TGGTCCTCTG AAGGAAAGAG	540
ATTATCCGAA TTACCGAATC TGAAT	565

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTTTATACTT TATCATTTCT AACTTAATTA TAGTCTTATT TTTAATAAAG TTCAATTATT	60
TATATGTAAA ATTCTCATC AGTAAAAAAT AACCGATCTC ATTTCTGAGA ATCGGTTTTTC	120
TAAATAAATC AAACCGATCA TTTACATAAC ATAAATTATG TAAATGATCA TACTACAACA	180
ACAAATCTTT GACTTTTCCA ATTTCACTTT TTGAATAAC CAGGTGAATC ATATCACCCA	240
GATACATTCT GGTGAGCCG TTAAGTGTTC GGCTCTTGCC ATTATGGACT TGAGTTGTGA	300
TGAGGACGTT GTGTGGTAAG TTGAGTTCAT GAACTTGTTT CCCAGCAATT TTATCAGAAA	360
CTGGTATTTC GATAAGTGTG ACTTCTCCTT CGCTAGATAC TTCTTCTGGG AAGCATTTTT	420
TCCAGCATGG CTTCATAGAC TGGCGTTCCT TTGAGCNAAT CCCTGATNAT TTTAGAAACC	480
AGAGTGACAG ACCAGTGGCT TAAGGTGCGA ATATCTCCTA CCATCTCAGT TACGAGAT	538

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CGTGCTAACC ATGAGAGCAT ATATTTCTC CAACTATTTT TATTTCAAAA AATCCTTACT	60
ATATTGTATC ACAATCAGAC AAAAAAGAA AAAGCAAATG ATAAACAAAT GCTTTTAANG	120
TTTTAAAAAA AGCTTCGAAA GGTTCTTCTT TATTTTTTAA NNGGAGAGAT AACGTTGATA	180
TCTAAATCGT GGTCAAAGCC GGCAATTTTC CTTTAGATGT GTATTGGTGA ATATCATAAT	240
CTAAATCAGT TTTAGGACTG CTCTCCAAA ATCCTGAGTC TGAGCCGTAG GACGGAATCC	300
AAACAGAGGT AAACCTGCCT GTATCAATAC TGTGTTCTTC CATGAAGTAG ACACCAACGT	360
AGATGCCGAT GTTTTGTAGCA CCTAGTGATG CTAGTTTTCG TCGAAAGTTT TCGACACCTT	420
CGTTCATATA GACATAGTTT TGTCTCCACG TCAGCCCATA GTAAC TAGGC TGTTAGGAGA	480
GCACATTGTA GAAACTTCG GCAGCCTTT	509

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CTGTTCTGTT	TGCGACGCTA	CTTGGTTGTA	GCATGGGGGT	GGTTTTAGAT	GGTCAGTAAG	60
TATCTTTTAT	TAGCAGTTAT	TTTCTCTGGC	TTGGTGACTT	GGATTCTCCG	TATGATTTCC	120
TTCATCTTAG	TCAAGTATAA	GGGCTTGCCCT	GCAATCGTTG	AGCGTTTTTT	GAAGTTCCTG	180
CCCGTTTCCA	TTATCTTTGC	CTTGATTCTT	TCAAGCGTAG	TGACAGGTAA	GGTTGGGAGC	240
CTTCCTCAAA	TTAAATGGCT	AGACTTCTTA	GCCGTCCTTC	CAACAGCTTG	GGTAGCCTTT	300
CGCTACCGCA	ATCTACTCGG	AACAGTTCTC	TTTGGAGTGG	TCTTGATTGC	CATCTTGCGT	360
TTGGTCTCTT	AAATTACCCA	CCAAAAAAC	TTATCACAGA	GATAGATATC	ATATAATGGC	420
GTAAATGCTC	CTTTTCTGTT	AAGATTATAA	GGTATTCTAT	TTTGGAGGAA	ATGACATGAA	480
AAAAATCGTT	AAATACTCAT	CTCTTGCTGC	CCTAGGACTT	GTTGCTGCAG	TGTGCTTGCG	540
GCTTGCTCAG	GGTGCTCAG	AAAGAAGAGA	AC			572

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

CTAGGTTATT	TAGTAAAAGA	CTAGAAGATT	TTCTTTTCCC	AATCGTCTTC	TGTACGGCGA	60
GGATAGAAAA	ACTCTGACTT	GTCGGGAGCT	TCCATCATTT	CCATCAATGG	TAGCATATCA	120
TAGGCCAGAT	TTAAGTTTGG	AATCTGGTCT	TTTTGCACCC	AAGAACTTC	TCCCTCTTCT	180
GAAGATTGAA	GGGTACCAGA	GAATCAGTC	GCCTTATAAC	AAATGACAAT	ATAGCGCCCA	240
CCTGTATCTA	GTGGCCAATT	TTTAATGCCG	ACAAGTTGAG	GATTTTGGAT	AGTCAACCCT	300
GTTTCTTCGT	AGATTTACAG	AATGACAGAC	TCCGCAAAAG	CCTCATCATT	TTCTACATGA	360
CCTCCAGGAA	AGGCATAACC	AGACCAGCGA	TTGTTTTTCAG	GGGCGCGATA	CTGCATCACC	420
ACGCGCTGAG	TTTCGANGTC	TTCCATCAGA	CAGATATTTG	TTTAAATTGT	TTAATTGGGA	480
ACGGGACATA	AATTTAC					497

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

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CTGAAATTTT GGAAGAAGAA ATCGGTGTAG ATACAGTCCA AAAAATAGGA CGCATCTTGA      60
TTTTGTTTAA ACAATCTAGC AAGAAAGAAA ATCGCAAGAT TTCTAAGAAA GTCAAAGAAA      120
TCTAAGATCG AAAC TCCAAA TAACTGTTTT TATAGAGAAA TAAAGGGGAC TAGCCTATGA      180
CAATCGAACT ATTGACTCCC TTTACCAAGG TAGAGTTGGA GCCAGAAATC AAGGAGAAAA      240
AACGCAAACA AGTTGGGATT TTAGGGGGGA ATTTTAACCC TGTTCACAAT GCCCATCTCA      300
TTGTTGCGGA TCAAGTACGG CAACAGTTGG GACTGGATCA AGTTCTGCTC ATGCCTGAAT      360
ACCAACCTCC TCACGTTTGA TAAAAAGGAA ACCATCCCTG AACACCATCG TCTCAAGATG      420
CTTGA                                         425

```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

CTGCTATCAA GACAGTATTA CCGCTGAAAG AAACAGCTTC ACTAGAAGGC GCAATTGAAA      60
AATAAGACGG GATCACGAAC TCCCGTTTTT CTATAAAGA AAGGAAATGG GATGAAAAAA      120
TTAGTCTTTG TCTGTCTGGG AAATATTTGC CGTAGCCCTA TGGCCGAGTT TGTATGAAA      180
TCAATGACAG ATAAC TACGA AATCCAAAGT CGAGCAACTT CCTCTTGGGA ACATGGCAAT      240
CCGATT CATA AGGGGACTCA GGAATTTTT CAAGAGTATG AGATTCCTTA TGACAAGAAC      300
AAGACATCGC TTCAGATTAG TAAGGAAGAT TTTGAAGCCT TTGATTATAT TATCGGAATG      360
GACGCTTCAA ATGTTCCGAC TTACGTCAGA TGTGTCCAGT AGACTGTCAA GATAAGAT      418

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ACTGTTTGAA	AAATATGATT	CGTGGTCGAG	AAATGAATTG	CATTTAAGCA	ATGTAGTTCA	60
GTATATAGAT	TTGGAAATTA	ATGATTTAAC	AAAATAAAGG	AGAAAAACA	TGGTTAAATA	120
CGGTGTTGTT	GGAGCAGGGT	ATTTTGGAGC	TGAATTGGCT	CGCTATATGC	AAAAGAATGA	180
TGGAGCAGAN	ATTACTCTTC	TCTATGATCC	AGATAATGCA	GAGGCGATTG	CAGAAGAATT	240
GGGAGCAAAA	GTTAGCAAGT	TCCTTAGATG	AGTTGGTTTC	TAGCGATGAA	GTTAGATTGT	300
GTTATCGTCG	CAACTCCCAA	ATAATCTTCA	TAAGGAACCG	GTTATTAAGG	CTGCACAGCA	360
TGGTAAAAAT	GTTTCTCTGT	TGAAAAA				387

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTTATGAAAT	CAATCATCAA	AATAATATTG	ATCAGGACTA	TTTAGGTAAA	TTATCTACAA	60
CGATTAAATT	GGTAGCAGAA	AAGGAAAATG	CCGTTGAGAT	CCTAGAACAC	TTGAATGTTG	120
TCCCTGTGTT	GACAGCCCAT	CCAACACAAG	TGCAACGCAA	AAGTATGTTG	GATTTAACAA	180
ATCATATTCA	TAGTCTTTTG	CGTAAATACC	GTGATGTTAA	GTTGGGGTTA	ATCAATAAAG	240
ATAAATGGCA	CAATGATTTG	CGTCGTTACA	TCGAAATTAT	CATGCAGACA	GACATGATTC	300
GTGAGAAAAA	ATTAAAAGTG	ACTAACGAAA	TCACGAATGC	TATGGAAATA	TTACAACAGC	360
TCCTTTGTGA	AAGCTGTCCC	TCATTTGACG	ACGGAGTATA	AGCGCTTAGC	GCAAGCGCAT	420
GGTCTGAATT	TAAACAGGC	TAAACCAATC	ACCATGGGTA	TGTGGATAGG	TGGTGACCGT	480
GAAGGAAATC	CATTGTGTAC	AGCAAAGAAC	TTGAAGCAGT	CTGCACTCAC	TCAGTGTGAA	540
GTCNTCCTGA	ACTTACTATG	A				561

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CGACCTAATC ATATTGATAC TGCATTTGCA TCAGCAGATT TGTTTGAGTA TAAATTACAA	60
TTAGCAGGAC AGACTTGGGG ATATTTAGAA TTTGAAACAA ATACAGAAAA ATATGGGAAA	120
GTATTGTTAA TTATAAAGGG TAAGAAGCGA CTTACGAACC AATTCCTTT GGTACAAAAA	180
AATAAGAGTG GCTACTTATT TGAATATGCT CAGATGAATA CACTTTATCT TAATCAACAT	240
TCTTCCTACA AAAATGATGA AGATAGTCAT TCCTTTCCAA TTCAGATGGA GTTAGTTTCT	300
GATGAAATGA TTCCAAGAAA TTGAACAAGC TACTAAAAAT TCCGAATATC CGAAAAATTT	360
ATGATTTTAA CTTATGANGC GGACTCCCGA AAAACAATAT TATATCTGTT AGATGTTTGT	420
TATGCCCTGA TGCCCGAACT GGTCCAGTTA CACTTGATTC CAGATTGTCC TGAGTATATC	480
CATCCAGTTC CGTACC	496

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCACCCTCTA GCAAGTGGTG CTAATTCCTA TAGCCTAGAA GAAAACGAAA TCATCTACCA	60
AAAGTTAAAA AACTTGCTTA AAAACTGATA AAATACTTGC CAACTTTTC AGAATCTGAT	120
AGACTAGTAT GGTAACAATC TATGGCTCGC AAAGAGACCA TGGCAGAAAG GAAATATTGC	180
AAAATGAAAA AAGATATCCA TCCAGAATAT CGCCAGTTG TCTTCATGGA CACAACACT	240
GGTTACCAAT TCCTTAGCGG TTCAACAAAA CGCTCTAACG AAACAGTTGA GTTCGAAGGC	300
GAAACTTACC CATTGATCCG TGTGGAAATT TCATCAGACT CACACCCATT CTACACTGGA	360
CGTCAAAAGT TCACTCAAGC AGATGGACGC GTGGATCGTT TCAACAAAAA ATACGGTCTC	420
AAATAATGAT AAGAGAACAG TTTCGGCTGT TCTTTTTTGT TTCTTGAAAT CAACTGCTGT	480
TTTCATGTTC CAGACTCATC TGTA	504

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```

CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAACCTT TAATGTCGAT GAGGCTAGCC      60
AATTCATTCA ACAATTTACA ATTACAAAAC AAATCGAACA AGTAGAAAAA CTATTAGAGG      120
AGTAGCATGG AACTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGCGCAGTAC      180
CTAGAAAAAT CGATAGCTTC CATTGAGAAG CAGACCTATC AAAATCTGGA AATTATTCTT      240
GTTGATGATG GTGCAACAGA TGAAAGTGGT CGCTTGTTGTG ATTCAATCGC TGAACAAGAT      300
GACAGGGTGT CAGTGCTTCA TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG      360
ATGAAGCCAG GCTCACGGGG ATTATCTGAT TTTTATTGAC TCAGATGATT ATATCCATCC      420
AGAAATGATT CAGAGCTTAT ATGAGCAATT AGTTCAAGAA GATGCCGATG      470

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(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```

CTTATACTTG CTTTTTTCCT TTTGAAAAAT GTTAATAAAT CGTTGGTAGT CTTCTCTAGG      60
CATGGACAGA TCAATATCGT CGTCCCAAGG GATAAAGCCC TCATGTCGAA CCGCCCCAAT      120
CAGAGTACCG TAGTTAATAA TATAGTTGAT ATTGTGCTTT TTACAGAGAG TATCAATATA      180
ATCCAAAATT TCTAATTCAA TTTGTTTGGC ATCTTCAATG GTTAGTTGTT TCATTTTAAA      240
CTCCTATGAT TTTTGAATT TATTTTAA GGCTAGGACA TGGTTTAAAA ATTCATAGAA      300
AATGCTATCT TTTGTGAAGA CAAGTAGACT AATATAAGAG ATAGCTGATA ACAAGACAAT      360
CAAACCAAGTA TTAATCAAAA ATGGCAAATT AATGACCATA TCCACAGGAT ACACGAAATT      420
AATCAGGAAA TACATTGCTA CAAAGGAAAG TGAAAAGAGA GAGTATCGAA CAGTATAGCT      480
AAAGATATGT CCAAGTGGA TGAGTTGTTT CTATGGATGA AATGAT      526

```

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```

ACCATATCAA TACTATCGAA AAGTACAAGG GATNCAGTCT CAAGGTCGCT GAGGAAGATT      60
TGAATGACCT AGACGATGGT GAATTTTACT ATCACGAGAT TATCGGTTTG GAAGTCTATG      120
AGGGTGATAG CTTGGTTGGA ACCATCAAGG AAAATCCTGC AACCAGGTGC TAATGATGTC      180
TGGGTGGTCA AACGAAAAGG CAAACGTGAT TTGCTTTTAC CTTATATCCC ACCAGTGGTT      240
CTCAATGTTG ATATTCCAAA TAAACGGGTC GATGTGGAAA TCTTAGAAGG GTTAGACGAT      300
GAAGATTGAT ATTTTAACCC TCTTTCCAGA GATGTTTCTT CCACTGGAGC ACTCAATCGT      360
TGGAAAGGCT CGAGAAAAAG GGCTCTTTGG ATATCCCAGT TNTCATAATT TTTCGAANAA      420
AATGCTGAAA AGG                                     433

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(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

CTGCAACTTG AATTTCCTCT TCTTGTTTCA AAGCAAGATA AACAAATCGA GCCCCCTCTTT      60
TTTCTAGCAA ATCCCCCATC TGGACAGATT GCATAAAGGA ACGAGAAGAA ACCTGATCAG      120
AATAAGTCTG AAATCTTCTT TCGTGAGTGT TTGTTAGTGC CATATACTTA CTTTCTATGT      180
TTTTTTCTTA ATGTTTACG GAAATCAAGA GCAAGTCTTA ACAGAGGATA GAGAGGATGA      240
GTGGGCATTG TAAATTCACC CAAGTATTCT TCAATCGTTG GATTAAATTT TTCCTTAAAA      300
TGATAAAGTC CACCATTGAG AGAGTTTTC AACCACCTA AATTTTGCCA GACCATACCT      360
CGCTCAAAGG CATAGCGAGC CGTTTCATAC CATGTTAAAA TTGGTGCATT GTAACGTTTA      420
AAATCATCAT CCATACCAGC ATATATATTG ACAGAGGTAG TACCAAATTC CAAACTCAAA      480
GTACCGCTAA AGGAATCTCG CTTGACCTAC ATCTATATAT TCCTGCAAGA AGGTCAATTC      540

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(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CTCAGGCTAA AAGAGTCCAC TGGACTCTTT TACTCCGTCC CATAACCAAT GACTTAATGG	60
CGCGTTTCAGC TAGATTATTG GAAAGGACCA GATGTCCGTC TTTCAAAATA GTCTTAAAGG	120
TTTCTTCATA CTTGAGGCTG TATTCAATTG CCCTTCCTAG TTTTGAACCC GATAAACTG	180
ACTGACGCCG GCACCAAGCA AAGAAATCTT CCATTAGGGG TTGGAGCTCT TCTTGACGTT	240
TCTGTAGTCG TTCATCAGCT GACAATGTCT CCCAGTCTCT TTCCAAGGCA AATAACTGAT	300
CACAATAGGC TAATCCTTTA G	321

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CTTGACCAAA CAAGGCAGTT GGAAATTGAT TTTGGAGGAT GAGAGCGCTG GAAGGGAAC	60
CTTCCCAATC TTGACTCAAG GTCNATATAT CGCAACATTT GACCAACAAG CGCCANCTAT	120
CGATGAAATC TTAAACTAT AATCAGGAGT GGAAGTATGA GAAATATGTG GGTGTAATC	180
AAGGAAACCT ATCTTCNACA TGTCGAGTCA TGGAGTTTCT TCTTTATGGT GATTTCGCCG	240
TTCCTCTTTT TAGGAATCTC TGTAGGAATT GGGCATCTCC AAGGTTCTTC TATGACTAAA	300
AATAATAAAG TGGCANTACT GACAACAGTG CCATCTGTAN CATAAGGACT GAAGAATGTA	360
AATGGTGTTA ACTTCGACTA TAAAGATGAA GCAAGTGCCA CCAGAAGCAA TTAAA	415

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CTATNAAATA GAGTGGTTCT CTATCTGCCA TGACCACAAA TNAGGACAAT GATACTTCTG	60
AACGTTTCAGA CTGCTATCGT AAAAGGACAG CGGGTGAGAC GCCCATGAAT GATCTAACCA	120
GTCATACCCA CGGAGGAAAT TATACAATAG CACGTTATCA GGAGGAAAAA TTTTGGAACA	180
AACAGTTGTA AAATATAGTC TGCAGTTATC AATGCTTAAT TTTTACAGG CGAAGATAAT	240

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTTGTCATCC TCACGAAAAT TCGGATTGTA AAGCACCAAG CCTTGACTCG TGATAGACTG	60
AATCATGCTT CTCTCATGTA CTCCTCAAGT CGTTTCATGG CTTCTTTGAT AGTCTCCATG	120
CTGGCTGCAT AAGATAGGCG GACGTAGCCT TCCCCGTAAC GTCCAAAGGC TGCACCAGGG	180
ATAAAGGCAA CGGCCTTCTT CTGAGCAAAA TCCTTCAGAA AAGCAAAGGA GTCTTGATTG	240
TAGCCCGCTG GAATTTTAGC AAAAATATAG AAGGCACCGT CTGGTTTGAT AATCTCAAAA	300
CCAAGAGCAG TCATTTTTCG GATGATATAG TCCCGACGTT GGATATATTC CTTCTTCATG	360
GGCTCCGCAT CGTTTTTACC AGCCGTCAAG GCTTCTACCG CAGCATGTTG CGCCATGGTA	420
TTTGCGGCAG TGACCAAGTT ACTGGTGA CTGATTAAC TGGGCTGTGA AGGTCNCANG	480
AGCAAAAATC AGCCCCAAC GCCAACCTGT CATGGCATG	519

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CTTCAGCTAT TCGTGGGATA TTAGATGTAC TTATTAGGG GTTGAAATCA TATGAATATT	60
ACCAATTTGT TTTCTATCAA GACAGGATGT GATGAACTG ATAGGCAACT GCAAAAATA	120
TTTTTTCAGT TGGATTTACA ATTGGGAGAA TTGACAGATC AACTAAGAAA ATTAGATTCT	180
AATTTTGTTT CTCGTAGTCA ATTTGTAGAC ACGTTGGATT TGAATGATGT AGAATATAAA	240
GAAATTTTAA ACTATTTTAT CTTCCATCGT AATGATAGTG AAGAAAGTTT GGTAGAATGG	300
TTATATGATT GGATTTCCAC AAATCGTTAT GAACTTCCCT AAAGAGTTTT CCGATTCCGT	360
ATGGCTCCAT AAATACCCAT GAAAGTGTTA CTGAAGTTTT CCGGAGAATG AATAACTAAA	420
AAACAGTCAT TAGTGACTGT TTTTATAGA AAAGAGTTTT TATATGTT	468

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

CTTGAATAGT CTCATCACGA AAATTGCCAT AACTGATAAA ACCAACCACC TTCACGCCAT      60
CCATCGCAAT CAATGTATTT TCTGGATACT TTTGACTAAA GAATCGACAT CTTTCTAATG      120
TCATTGTATC CTGAAATCC GCAGGCAAAA GGTCATCATA AGACTCTCTC CACGTTTGCC      180
AGTGAACGAG GGATTTGCCT TCTATCTCTT CAGGAGTTNC CATAGATTG ATAATAACCG      240
TCATTATTTT TCTCCAGTC TNCTCTCAA ATACCATATT TAATACTATC AAAATATTTA      300
CCTTGATAAT AACGAACTTT NGGAATATGA GCTNCTTTTT TCATNCTTAA TTTTTCAGCA      360
AGTTTCATCA TACCAAGATT TCCTGACCAA GTTGTCAAAA CCAGATGCTC CAACTCCAAG      420
TAATCCTGAA ACGTCCTATC TATCCACTGC AACATAGCAA CTTTCCCAAT ACCAGTGTC      480
CAGAATTTTT TATCATAAAT ACCAATTCCC AATCCATCCA TCTTGTTTCC TTTACATACC      540
CAATA

```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

CTTGATTGTG GAAGAAGTCC GTGATCGCTA TGTGGGCAAA GTCGATGCCG TTTTTCATAA      60
CGGCGATTCT GAACTACGTC CGGATTCTCC ACTTTGGGAG GGCATCCGCG TTGTTAAAGG      120
GAACATGGAC TTCTACGCCG GCTACCCAGA ACGTCTGGTG ACTGAGCTTG GTTCGACCAA      180
GATTATCCAA ACTCATGGTC ACTTGTTTGA CATCAATTTT AACTTTCAA AGTTGGACTA      240
CTGGGCTCAG GAGGAAGAGG CCGCTATCTG CCTCTATGGT CACTTGCAATG TGCCAAGTGC      300
TTGGTTGGAA GGCAAGATCC TCTTTCTAAA TCCAGGCTCT ATCAGTCAAC CACGAGGTAC      360
CATCAGAGAA TGTCTCTATG CTCGTGTGGA GATTGATGAT AGTTACTTCA AAGTGGAATT      420
TTTGACACGA GATCACGAAG TGTATCCAGG TTGTCCAAGG AGTTTAGCCG ATGATGCCAA      480

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GGAGTTGAGA CTTTCTGTTG GGGCAGAGAA CTTTTGA

517

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CGTAACCATT AACTATGAGG TGGTTTGCCT CCTCAGCGAC CGTATTCCGA GAGAATATTA	60
TTAGAAAAGA AAGGAGTGGG GCATGAATCT ACATCAACCC TTGCATGTCT TGCCTGGTGT	120
GGGACCAAAG TCAGCAGAAA AATACGCCAA ACTAGGAATT GAAACTTGC AAGATCTCTT	180
GCTCTACTTT CCTTCCGTT ATGAAGACTT CAAAACCAAG CAGGTGCTGG AACTAGAAGA	240
CGGTGAGAAG GCAGTTCTTT CTGGTCAGGT AGTGACTCCT GCTAGTGTC AGTATTATGG	300
TTTCCAAGCC GCCAATCCGC CTGCGTTTTT AGTCCTCCAA GCCAGGGAAG AAGGTTTCGT	360
TTTTTTTGGC GGGTGAAATT TCCTTTTAA CCCAGCCCCC TATCCTTGGG CTTGAATAAA	420
AAATTAGAAA TTTTGGGGAA CCAACCCCTT TGGCTTGT	458

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTTACTAGT TTACTCAATC TTTACATCGT TC'TTTCGGCA GTTCAAACCTC AGAATCCACA	60
GCACAGGTTA TGCAATTACT GTCTGAAAAT ATGTTAAAAA CCATTCAGTC ACTTTCGGTC	120
TGGCAGATTT ATTTGCTTGG TTTTGAGCGA ATCTTGGCGC TTGGTTTCCA ATTACTTTTG	180
ACAGTTTGGG TTTACCAAGC TG'TTCGCCAG AAGAAATGGA TTTATCTCCT AGCAGCCTAT	240
GGCTTGCATG CCTTCTTTGA TCTGGCACCA TCTCTTTTCC AAGTAGGCTG GTTGACAAAT	300
CCAGTCTTGG TTGAAGTGAT TCTAGCACTG GAGCTCGTTC TGGTCGCCTA TGGAAACCAAG	360
GAAATCTTTT GTAAAAAATC ATAAAAAGGG GGGAACCTCT TTTTCTTATG CAAAATCCAA	420
ACAAGGTATT TTTATGGTCG TCAAATGTCT CTAAAAATGG TATAATGGAA TGAATTTTGT	480
AAAAGGAAGA ATGACATGTC TGTAAGAGAA AAAATGCTTG AAATCTTAGA AGGAATTGAT	540

ATCCGTTTTA AGGAACCCTT GCATAG

566

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

CTTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCT GAAAAATTTA    60
TTGTGGATGG TTTCCAAGGG ATTCGTGACC CACGTGGCAT GATGGGGGTT CGCCTTGAAA    120
TGCGTGGTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTTGCGT AAGACGGTTG    180
AGCGTGCAGG TGTTTCAGGT GAAAATGTTA TCATTTCACT ACTAGCAATG GTTCAGTCTG    240
TTTTGAACGA AGGGGAACGT GAATTTGGTG CTACAGTGAT TGATATGGGG GCAGGTCAAA    300
CGACTGTCGC TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGTGG    360
AGATTATGTA ACTAAAGATA TCTCCAAGGT TTTGAAAACC TCTCGCAAAT TAGCGGAAGG    420
CTTGAAACTG AATTACGGGG AACCTATCCG CCTCTTGCAA GCAAAAAACT CCATTAAAGT    480
TATTGGAGAA TTAAACCAGT CAAAGTGACG GAACCTACTT GTC                      523

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(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

CTGTGATTTT AGAGAAGAAA TCAAGTGCTG TAACAGAAGT AAGATGTAAT TGTATGTAAA    60
GGAGACGTCA TGTAAATAG TATTGTAACC ATTATTTGTA TTGCCCTTAT CGCGTTTATC    120
TTGTTTTGGT TTTTCAAAAA GCCTGAAAAA TCTGGACAAA AAGCCCAGCA AAAAAACGGA    180
TACCAAGAGA TTCGAGTGGA AGTCATGGGA GGCTATACTC CTGAGTTGAT TGTCCTCAAG    240
AAATCAGTGC CAGCCCGCAT TGTCTTTGAC CGCAAGGATC CTTCAACATG TCTGGATCAA    300
ATTGTTTTTC CAGATTTTGG TGTACATGCG AACCTGCCAA TGGGGGAAGA GTATGTAGTG    360
GAAATCACGC CTGAACAGGC TGGAGAGTTT GGCTTTGCTT GTGGTATGAA CATGATGCAC    420
GGCAAGATGA TTGTAGAGTA GGTGGAGACT ATGACAGAAA TTGTGAAAGC AAGCTTAGAA    480

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AATGGCATTG AAAAAATCCG TATCCGAGCT GAAAAAGGCT ATCATCCACC CATATCCA 538

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CCTCAAGAAG	TCCGCGATAC	TTACGAAAAT	ATTTTGTAGA	GAATCGAACC	GCAAGGTTTCG	60
GTTTTCTTTC	TCTTTTGTGTC	TATAATTTGG	TATAATAAAC	AGTATGAAAA	TCGTATCAGG	120
AATCTATGGG	GGACGTCCCC	TCAAGACACT	AGAAGGCAAG	ACAACAAGAC	CTACTTCGGA	180
TAAGGTTAGG	GGAGCCATTT	TTAACATGAT	TGGTCCCTAC	TTTGAAGTGG	GACNAGTCTT	240
GGACCTTTAT	GCAGGTAGTG	GTGGTTTATC	TATCGAAGCA	GTATCGCGTG	GCATGTCCAG	300
TGCTGTTTTG	TGGGAGCGAG	ACCGTAAGGC	TCAGACCATC	GTGGCTGAAA	ATATCCAGAT	360
GACCAAGGAA	GTGGGAAAAT	TTCAACTCCT	CCAAAATGGA	TGCAGAAAGG	GCATTGGAAC	420
AGGTTNTCTG	GGGAATTTGA	CCTCGTTTTT	TTAGACCCTC	CCTATGCCAA	GGAACAAATC	480
GTAGCAGATA	TTGAAAAAAT	GGCTGAGAGA	GAGCT			515

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGANACAA	ACTTTACAGA	TCAAGTCGAT	ACGATGATTT	ATGTTGATAA	AGAAGAAAAA	60
GAAACTATTA	AAGCTGCACT	TGTGGAGTTT	TTTAATGGAA	AAGTCACTTT	AAC TGACCAA	120
GGTTTACGAG	AGGTTGAAGT	TCCTGTAAAC	TTAGTGTAAG	CAATGAATAA	TACAGCGTTT	180
CGTTGACATT	CTCACAAC TA	CTTTAGCGAG	CAAAATAAAA	AGATGCGTAC	CAAAATATAC	240
TAGAAAATGA	AGCAATTCAA	ACGAAACCTG	ATATCGTTTT	CCTTCACACC	TATTTACTAG	300
AATTAAC TGA	ACGCAATCAC	TTGAAAATTA	ATGACTTTTG	AT		342

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

CTATTAGCGA CTTTCTCTGA AATATGGTAT GATAAAGGAT ATACAAGGAG ATAAATGAA      60
TAATAATTTA CTGGTATTAC AATCCAGACT TTGGTCTGGT TGATGGTGCG GTATCGGCTA      120
TGATTGGAGT GGCTTTAGAA GAGTCTCCAA CCTTAAAAAT CCATCACTTG ACGCACGATA      180
TCACGCCTTA TAATATTTTT GAGGGGAGCT ATCGTCTCTT TCAGACGGTG GATTACTGGC      240
CTGAGGGAAC GACGTTTGTA TCGGTTGTGC ATCCAGGTGT CGGTTGAAA CGTAAGAGTG      300
TAGTTGCCAA GACTGCTCAA AAATCAATAC ATTGTCACGC CAGATAATGG GACGCTTTCC      360
TTTATCAAGA AACACGTTGG CNTTGTANCC ATTCGTGAGA TTTCTGAGGT GGCCAAC      418

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(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

CTCTCGCTTT TCTCATAGTG GGAGGTAAGG ATGGAATTAC GCAGACCAAG ATTAGCGGAT      60
AAGAAAGCTG TTTTAGATAT GATGACAGAG TTTGAAAAGA GCCAATCAGC CCATGATGGA      120
GGATTTTGGG ATACAGAGAA TTTTGTGTAT GAAGAGTGGT TGGAAAGCAA TCAGGAACAG      180
GAAATGGGGA TTAATCTGCC TGAAGGATGG GTTCCTGCAA TTCAGTTAGT GGCTTTTCT      240
GAGAAAGGTC AAGCAGTTGG ATTTCTTAAT CTCCGGTTGC GCCTCAGTAA CTTTCTACTA      300
GAAGAAGGTG GGCACATTGG CTAATCCATC CGTCCATCTG AAAGAGGCAA GGGTTATGCA      360
AAAGAACTCT CCGTCAGGGC TTGCAAGTTG CTAAGGAAAA GAACATCAAG AAAGCTCTGG      420
TGACCTGTAG CGTGAATAAT CCTGCTAGCA GAGCATCATT CTA                        463

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(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTCTTACGTG ACCAGAACAT GCTACTTCCC ATCCGAGAAG CCATTCTATC TGGCTTACCA	60
GTGTTTGGGA CCTGTGCGGG CTTAATTTTG CTGGCTAAGG AAATCACTTC TCACAAAGAG	120
AGTTATCTAG GAACTATGGA TATGGTGGTC GAGCGTAATG CTTATGGGCG CCAATTANGA	180
AGTTCTNCAC GGAAGCNNA TGTAAAGGAG TTGGCNAGAT TCCNATGACC TTTATCCGTG	240
GTCCGATTAT CAGTACTGTT GGTGAGGGTG TANAAATTCT AGCAACAGTG AACNATCAAT	300
TTGTTGCNNC CCAAGANNAA AATATGTTGG TAAGTCCTTT TCATCCAGAA TTGACTGATN	360
ATNTGCGCTT GCNCCAGTAC TTTATCAGTA TGTGTAAAGA AAAAAGTNGA GATTGAATTT	420
CTCCAACCTT NCCACNTGTA ATNNNCAATN NCNATGTATT GGAGTACGGA CGCAG	475

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCTTCAAAAA TTATTTGATG CAACCTTAGA CAATCCAGAA CTCACGCAA CATTAGTGCC	60
TTTAGGAGAT GGTATTCTCA TGCTTCGTAA AAATGTAGCA GATGTTCAAC TGTCTGAAAG	120
CGAATGATTT TCAGAAAAAT TTAAGAAAAA ATAGTAAAT AGATAGAGTA ACACTTATCT	180
CAAAGGAGTA GACATGAAGA AAAAATTATT GGCAGGTGCC ATCACACTAT TATCAGTAGC	240
AACTTTAGCA GCTTGTTCGA AAGGGTCAGA AGGAGCAGAC CTTATCAGCA TGAAAGGGGA	300
TGTCATCACA GAACATCAAT TTTATGAGCA AGTGAAAAAC AACCCTTCAG CCCAGCNAGT	360
CTTGTTAAAT ATGACCATCC AAAAAGTTTT TGAAAAACA ATATGGCTCA GAGCTTGATG	420
ATAAAGAGGT TGATGATACT ATTGCCGAAG A	451

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

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CTATGGATAA GGCACCTTGCT GACCTCAAAA CATCAGGGCA CTTGCCTATT CCGCGACACC      60
TACGTGATGG GCACTACANT GGAAGCAAGG AACTGGGGAA TGCCCAAGAC TATCTCTATC      120
CACACAATA TCCTGNAAAT TGGGTCAAGC AAGACTATCT GCCACAAAAA ATTCGTAATC      180
ATCACTATTT CCAAGCAGAA TATACTGGTA AATATGAACG GGCTTTGGCT CAAAGAAAGG      240
AAGCTATCGA CCATTTGCGA AAAATCTGAA ATCCTTTTCA AAAAATTGCA CTTTCCTCTT      300
GATTTTTTTT GAAAAAGTGG TATCATATAA ATATAGAAAC GCTGTGGTGT ACGACTTCAC      360
ACTTAAGTGT TGACCGACTA TTTTGTGTAT TATTANGGAA ACAAAGTCT TCTGTCAGCA      420
TGTAGGCCGT CTCACACGGA AACAGCTTCA GTT                                     453

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(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

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CCGTAGTACA GGCACAAAAA GATTTGAAA ATAGAAAAAG AAAAGCCAAG AAAAAGGCTC      60
AGAAAACGAA ATAAATAAGG AGGAATCTGG TAATGGTAGT ATTTACAGGT TCAACTGTTG      120
AAGAAGCAAT CCAGAAAGGA TTGAAAGAAT TAGATATTCC AAGAATGAAG GCTCATATCA      180
AAGTCATTTT TAGGGAGAAA AAAGGCTTTC TTGGTCTATT TGGTAAAAAA CCAGCCCAAG      240
TGGATATTGA AGCGATTAGT GAAACGACTG TTGTCAAAGC AAATCAACAG GTAGTAAAAG      300
GCGTTCCGAA AAAAATCAAT GATTTGAACG AGCCTGTGAA GACGGTTAGT GTAAGAAACC      360
GTTGACCTTG GTCATGTGGT TGATGCTATT AAAAAAATAG AGGAAGAAGG TCAAGGTATT      420
TCTGATGAAG TC                                     432

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(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATCAAGA AATTCCTTTGA AGGAACGACA GATACAGCTG AGAACTATAT CAAGTCGGCC	60
CTTAAAATGT TGGTCAAATA GGAGCAGAGA ATGACAAAAC GTTGTTTCGTG GGTCAAGATG	120
ACCAACCCGC TCTACATCGC CTATCATGAT GAGGAGTGGG GTCAGCCCCT CCATGATGAC	180
CAAGCATTGT TTGAGTTGTT GTGTATGGAA ACCTATCAGG CAGGCCTGTC TTGGGAAACG	240
GTACTIONAACA AACGCCAAGC TTTCCGAGAA GCCTTTCCAT AGCTATCAAA TTCACTCCAG	300
TCGCAGAGAT GACTGACACT GAATTGGAAG CCATGCCTGG AGAATCCCAG CTATCATTC	360
GAAATAGAGC CCAAGATTTT TGCTACACGC CGCCTAACGC CCCAACCCCTT TCCTACAGTT	420
ACAGGCAG	428

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CTATTAGATG GTATTGACTG CCCAGACACT TACGGATCTA GCTGAGACAG GGAATTGTCC	60
ATAACCTTCC TCATCAATTG TAACTTGACC TTGGTGGTTA CCAAGTAAAT CTACAAAGGT	120
TTGATTAGTC CATTCCTGAC CGACAAACAT TGACTTGCTG TTTTCTTGGT CATTTGAAAT	180
CAAGACTGCG ATTGGGGATT GATTTCAGC ACCTGAACGT ACCCAACCGA TACAGTTAGC	240
ATGGTCAAAG TAGTCATTTT GTTCTCCATA GGCCAAATCT TTTCCGATGG CTAGGAGGCG	300
GTCAAGGATT TCTTTGAAAT CTTGTTGAGC ATACTGGCCT GAAATCCCAT AGTAGTCTCC	360
GTAAGAGACA CATGGAAGGC CGTCTTGCG TAACAAATG AGGGCATAGG CTGCTGGCTT	420
GAACCATCT TCAACGGTAG ACTCAAGGC TTGTCTCGT TGGGTATCGT GGTGTGTCGAC	480
AAAATCACAG ACTTGTGAGG CTTGAGTTCA ACCAGGCT	518

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTCTGTCCTT TTACCTGAGA GTTTGAGCAG TTGCCTGCCT TGCCCCCTTCG GTGCCTTTAC	60
GGTCTCTCCA GAGTTCCGTC CATTTACAGT CATGGAAAAT CAAACGATTC CCCACTTCTA	120
TTAAACTTCA TTCGGTGTG GTATTTAATT GATTCTAATT TTACAAAAA TGTGGGCTTT	180
TGTCAATGTG TTTATTAGTA AAAATTAGTT CAACAGTTTT TACTTTATAA AGTCCAGAAT	240
ACTGCTATCC TTTAAAAGTG ACAATAGTCG CACCACTGCC TCCAGCATTT TGTGGGGCAT	300
AGCCGAAACT CTTGACATGT TTGTTTCTTT GCAAGTATTT GGTAACCTCT TCACGGATGA	360
CTCCTGTTCC GATACCATGG ATGATATCAA CTTGAGCCAT ATTGTTAAGC AAGGCTTGGT	420
CGAATGAAGG TATCTAGCTC ATTCATGGCT TCTTCATAGC GCTTGCCTCG AAGATTCACT	480
CTAGCTTGAG TCCTCGCCCA GAAGTTCTG	508

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTTGGGCT CTCTTCTCAG CAACTTCCCT GCTTTCACCT TTGGTCTTGA TAGGTGANAA	60
CGTAATATNT CCAATCANNNG TCATATTAGG AAANAGTTAA ATTGTTGGAA AACCATGCCC	120
ATCTTCTCAC GCATGGGAAA CAGGTCATTC TTCTTGTCG TAATATCGAC TCCCTCAAAG	180
ATAACCTTCC CCTTGGTTGC TTCCTCCAAC AAATTCATAT AGCGAAGCAA GGTAGATTTT	240
CCACTCCCTG AAGGACCGAT GATAACGACA ACTTCTCCTC TTTTAATCTC GAGGTTGATG	300
CCCTTCAATA CTTCAATTCTT TCCAAAAGAT TTATGTAATT TTCAATTTTT ATCAAGGTTT	360
CTGTCATTAT TTCTTATC	378

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTGGCCAGCC	AGATAAACCT	CGATACGGCT	TTCTGCTCGT	TTGATGCGTT	GCAAGAGTCC	60
GCCCATACGG	ACGTCAACTG	TATCCAAACC	AAAGACCTTG	TTTTATTTC	GCCAGTGGTG	120
ACTAAAGAGG	GCATGGAAGT	CTTCAATTTG	GCTTCTAAGT	TCTGGTAATT	CTTGTCTGGC	180
GATTTGTTGT	AAACTTTCTT	TATCATCCGC	TTGGTAGGCA	TGACGAATGC	GTCGTCCCAC	240
ATCTACTTTG	CTACTTAAAA	TAGCATTCAA	CTGGGCCTGA	GTTTCAAAGA	GATAAGCATA	300
GTTTCCAGCT	TTTTCTTTAA	TGTCAGCAAT	AGTTCCCGCC	GCCTGAGCGA	AGTGTGGCTT	360
GTCTGTTTCA	GGTGTCTATG	GTCGGTCAAG	TATCGGACAG	AGAACATCCT	GATAAAAGAC	420
ATAGCGGTTG	GGATTGATGC	CACTGAGATT	ACCTGGTAGG	TCTGGTAAGA	GGTTGGCAAG	480
ATCAATCTGC	ATAAAATCCT	CAACCGTTAG	ACCAGTATTG	GTCTTGAAAT	GCGCAGACAA	540
ACTATCTAGG	TCATTGCGAT	AGATCAAGTT	ATCGATACCG	TCGACCTCGA	GGGGGGCCGT	600
ACCCAGATTT	GCAAGCTTGG	TAGGATAAAG	AACTGGGCAG	TTTCACCACC	ATTGTCTCCC	660
CAACCCGTTA	CGATGACTTC	TTTAATCTGA	TTGGCACGGC	AGGCTTTATT	AGCCTCGATA	720
GCCACTAGAC	GGCTAAAATG	G				741

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAACTCGATT	TGAGAGAAAG	TCCAATAAGT	CTTTCATATA	TAAAACGCAT	AGTAGCAAGA	60
GTTTCTACAC	CCACTATTAT	GCGTTTTTAT	CATTTTGAAA	TCTACTGCTA	ATCAATGAAG	120
AAGCAAAGAT	CAAACTAGGC	AGCTAGTTAC	AAGTTACGTA	AGCGCGTCAT	AACAAGGTAT	180
CTATCCTAAT	TCCCCAACTT	CCAGTATACT	AGATAAAAAA	TAATTATCGG	AGGAAAGGTA	240
TTGTACTATG	ATAATTCAAC	TAAGTGATTT	AGGTCAAGTT	CACCTTGTTT	GTGGCAAGAC	300
AGATATGAGG	CAGGGAATAG	ACTCATTAGC	CTATGTAGTT	AAAACCCACT	TTGAATTGGA	360
TCCTTTCTCC	GGTCAAGCCT	TTCTCTTTTG	TGGTGGACGT	AAAGACCGCT	TTAAAGCCCT	420
TTACTGGGAT	GGTCAAGGAT	TTTGGCTACT	ATATAAACGC	TTTGAGAACG	GAAAAC TGAC	480
TTGACCAAGT	ACAGAAAAGG	ATGTCAAAGC	TCTCACACCA	GAACAAGTAG	ACTGGCTTAT	540
GAAGGGCTTT	TCTATCACTC	CCCAAATATA	GTGGATTTAA	ACTAGAATAG	TACACCCCTA	600
CTTCTAAAAC	ATTGTTAGAA	ATCGATTGTA	CTGTCTGAT	CAATTTGTCC	TGTTCTTATT	660
TCATTTTACT	ATAGAATCCA	TCTGAAAGCC	GTTTATGATT	TCTATTGAAA	TGAAGACCGT	720
CCATTTTAGT	AGACTAAAGG	ATTACTCAAA	ACTTCGAGAA	GGAAGACAGA	TGAACTTGTT	780
TCTTATAAAA	ATGTTGTCTG	AAACTATTCTG	CTTTTTTCCA	GAAATTTTAG	AGGAAGAAAA	840
CTTTATGAGG	AAAAAGGAGT	TACTCAAATA	ACAATTCAGG	ATTAAAAATA	GACAGTTGAG	900
GAGCGGAAGG	TATAAATTAA	GTTTGCTACT	GTATAATGGA	TTTAAATCAC	TCAGCAGACA	960
GAACGAATAC	TCTTCGAAAA	TCTCTTCAAA	CCACGTCAGC	TTCCGCTTGC	CGTAGATCCA	1020

TAGGGGACTG	GACTTCATCA	GTTCTATCAA	CAACCTCAAA	ACAGTGTTC	GAGCTGACTT	1080
CGATCAATTT	TATCTGCACC	TCAAAGCTGT	ACTTTGAGCA	AGCCTGACGA	CTAGCTTCCT	1140
ATTTGATTTT	CATTGAATAT	CAGAACTCA	TTCTCCATCA	AATAATTCGA	CTGCGTCTAA	1200
TAATTTTGG	TCTGGCACGG	TGTCAGAAAT	AAAGGTTGTG	TATTTGGAGA	GGGGATTAAT	1260
TTTAAAAAAT	CCAGTCTTGT	AAAATTTAGA	ACTATCAATC	AGTAAGATGG	TTTCATGGGC	1320
TTTGTCAATA	ATATTCTTTT	TTGAAATAG				1349

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CTTTTTTATA	AGCAATTCAA	TTTATACTC	ATCTGCTTTC	AAAAAGCATT	CTAGTCCATC	60
TCCGATTAAC	GATGGACTTT	ATCACCTCCT	TCTCCAATCC	TTGTATGACA	TCTTGAAGTT	120
GATTCATGAC	ATCTTCCAAA	ATTTCGAAAGG	CTTTATTCTT	AAATCCACGT	TTACGAATCT	180
CTTTCCACAC	TTGTTCAATG	GGGTTTCATCT	CTGGTGTGTA	TGGAGGAATA	AATGCAAAAC	240
CAATATTAGT	CGGAATCTTT	AAGACACTTG	ATTTATGCCA	TATAGCATTG	TCCATAACGA	300
GTAAAAAATA	ATCATCTGGA	TAAGCTTGTG	AAAGCTCTTC	TAAAAAGGCG	TTCATCCACT	360
CAGTATTACA	TCTACCAGCT	ATTAAGAAAA	AATGATTCCG	CCTGTTATGG	GCATCAACAG	420
CTCCATAACA	ATAGTGAAAT	TCTCGTATAT	AGTGACTATG	GACATGTGGA	CCTACTCCTA	480
TTGGAGACCA	ACAAGATCCC	AGTTTACTGA	TTCTACCGAA	ACCAGCCTCA	TCTTGGTACA	540
TCAAGCGAAC	CTTATGAAAA	CGTCTACTGG	TTTAAATCGC	TTTCTTGTCT	TCTTGAATTG	600
AGATTTTATT	TTTAGACGCG	ACAATGGTTT	GAGCGTCTGC	TTTCTTAGGA	TGTTCTGGAC	660
GTGGCATAAT	ATTTGCGCCAG	CCATGGCGCT	TCAACAGTTG	ATAGAAGGCA	TCACGTGTGT	720
AGGAACGACC	TAACTCCTTT	TTATAAGCCT	GAAATAAGGC	ATCAATTGTA	ACAAATTCTC	780
CTGCCCTCTGT	AGCCTTCAAA	TGGCGGGCAA	GAAATACTTT	CTCTTCCTCA	ACTGTCATAT	840
ATGCATGGTT	ACACCACCAC	TTTCCTGATA	GAGTTGTTCA	CATCTTATTT	CAAACACTA	900
TAAAAGTTCT	ATAATCTCTT	TATAAGATTT	GCCCATCAGA	CGAAATATAA	TAAATTGAAA	960
CTAGAATAGT	ACACCTCTAC	TTCTAAAACA	TTGTTAGAAA	TCGATTTGAC	TGTCCTGATC	1020
GATTTGCCCT	ATTCTTGTTT	CGTTTACTA	TAGAACGATT	TGAAGGCGTT	TATGATATTG	1080
AGCTGTACGA	GAGTCTTTTA	AAAGTGTTTT	GATGGCTTGG	ATTTCTTCTT	TAGTTGATTT	1140
CATATCACTA	TTATATAATG	CTTTTGTATC	TTTAGTTTAG	TATTATCGTA	GAAAATGGAC	1200
TAGGTGCTAT	GGATACACCG	GATGAGAATG	GTTATGTAGC	AGATGACTAT	CGGATTACTT	1260
ACTTAGAGGC	CCACATCAAG	GCCATGCGAG	ATGCCATTTA	CCNAGACGGG	GTTGACTTGC	1320
TTGGTTATAC	GACTTGGGGC	TGTATCGATC	CAGTTTCAG			1359

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

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CTAGTATTTT CGTTGTGNTT AGTTTGTCTG CCTATGGAGT TATTGCCTAT GTGCAAGGTC      60
AGNTGGATAT TCCTCTAGTG ATTCTGGCCA TGATTGGTGG TTTGCTCAGT TTCTTCATCT      120
TTAACCATAA GCCTGCTAAG ATCTTTATGG GTGATGTGGG AAGTTTGGCT TTAGGTGGAA      180
TGCTGGCAGC TATCTCTATG GCTCTCCACC AAGAATGGAC TCTCTTGATT ATCGGAATTG      240
TGTATGTTTT TGAACAACAACT TCTGTTATGA TGCAAGTCAG TTATTTCAAA CTGACAGGTG      300
GTAAACGTAT TTTCCGTATG ACGCCTGTAC ATCACCATT T GAGCTTGGG GGATTGTCTG      360
GTAAAGGAAA TCCTTGGAGC GAGTGGAAGG TTGACTTCTT CTTTTGGGGA GTTGGGCTTC      420
TAGCAAGTCT CCTGACCCTA GCAATTTTAT ATTTGATGTA AGAATGGCAC CCTGATGTTT      480
TAGGGTGTTT TTGTGTTTAA ATACACAATG AAAATCAAAG AACAACTAG AAAGCTAACT      540
TTAGGCTGCT CAAAACATAG TATATTGAAA CTAAAATAGT ACACCTCTAC TTCTAAAACA      600
TTGTTAGAAA TCGATTTGAC TGTCTGATT ACGATTTATC CTGTTCTTAT TTCATTTTAC      660
TATACCATCA ATAAGTGTTG AAAAGATCGT TGACAGAACT GACCAAGCCA GATCATCTTT      720
GTAACCACTT TGAGCTTGTA GCATATTTGT TAATTGAGCA AAGGCGCTAG AAGAGTTTGC      780
TGGGTCAGCA GTTGCGATTT TTCCTTTTAG TTCAGGTTTG AGAAGGTCGC TATATCCTTC      840
GATGTTTATG CCTTTAGTTA AATCAGGGTG GACGATTAAA AACTACCAT CTAGTGATA      900
AGGAGTAGAG AAGCCAGTTG TGTTTGTATA TTCTTTGATA ACATTATCAT TTTCTTTTGA      960
AATATAGTTT TCAAAGAGTT CTCCGTGGGT AGCATATTGT GTTATAAGAA CCACCAAAGA     1020
TAACATCAGC TACAGGAACT TCTTTTCTG ACCTAGTTT TTGAAAAGTT CTCCAGTACC     1080
AG                                                                                   1082

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(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

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CTGGACTTGA TAGGCATCTT TGTAATCCTC TAAAGCCTCT TTCATCAAGG CACTACCAAT      60

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TCCTTGACGC	TGATAGATTG	GTAAAACGAT	TAAATCCTGA	ACCAATACTG	ATGAGAATCC	120
ATCTCCAACC	AAACGAATCA	AGCCCACCAC	AGCATCACCA	TCAAGTGCCA	CATAAATTAC	180
TAATGAATGA	GATAAGGCCT	GCTCCAGCAT	CTCTGGTTGA	TGGGTATAAT	TAGTCCAACC	240
GACAGCCTGA	TAGACATGTA	AAACATCCTC	TAGCTTGACA	ATTCTTTGCT	TTTTAATAGT	300
AATCATCTCA	ACACCTCTTA	AAGTTCTCTC	AAGCTCTTGT	ACTGCTGTCC	ATTTTATATCA	360
AAATTTTCAG	GACGCAACCA	TGTTTCCAAA	CGATCTTTGA	CTTTGGGCCA	GTCCTTATCA	420
ATCATAGACA	ACCAATCCAT	ATCTCTCGTA	CGCCCCTTAT	AAACCACTGC	CTGACGGAAG	480
GTTCCCTTCAT	AAATAAAGCC	CAAACGCTCC	GCAGCACGTC	TGGATGGCAG	GTTAAGAGCA	540
TCGCATTTC	ACTCATAACG	ACGATAGTTA	AGCTCTTCAA	AGACATAGCG	AGCCAGTAGA	600
TACTGGGCTT	CTGTCCCTAT	CCGTGTCCCC	CTGAGTTTTG	GAGAAAAAGT	GACAGCTCCC	660
ACTTCTATTA	CTCCGTTACT	GGTCAATACG	CATGAGAGAA	AAATTCCCAA	AGCCTTACCA	720
GTTGCCTTGT	CTATGTAGTA	AAAACGGTCC	TTACGAGCCA	ACATCTGACT	ACTATAGTAG	780
ATTGAAACTA	GAATAATATA	CCTCTACTTC	TAAAATATTG	TTAGAAATCG	ATTTGACTTC	840
CCTGATCGAT	TCGTCCCTATT	CTTATTTTCAT	TTTAATATAA	TTGATAGTGG	TCGCCCCAGC	900
CAGATACCTT	ATCTGCTATC	CATTTAGGAA	CCCCTAACTT	AAGCAATCCC	CATAATCGTC	960
TCGATTTCCT	CTTCCATTGC	TTCCAGATAA	TCACTCGTAG	GCGAGTACGC	AAGCGCTCAT	1020
CTATGTTAGT	GACTATACTT	TTCATATTTA	TAATTCATTG	CTTTCGTTTC	ACTCAAGGCA	1080
CAACACAGAA	TGAAAAAGTG	TTGTGATCTT	TATTTTGTTT	TATAATAATA	GTGAGAAAGC	1140
CTATCACTAC	TACAAATCAC	GGGGAGGTGA	ATAAGTGAGT	GGTACAGCCA	CTACCTCGCA	1200
TATTTTGTCA	CATCATTTAA	CGGTACATAA	TAAGTTGTAC	CATCTGAATA	AGTTGCTACA	1260
ATATCATTTG	CATGCTCTCC	TTACCTTTTA	GCAAAGGTTG	GAG		1303

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTCTTCAATC	AACTCACGCT	TTAGGGCTTC	CTGATGATTT	TCACCTGCTT	CAATTTCTCC	60
ACATGGTAGG	AACCAAGCAC	CATTTGGTTC	TTGAACAAGA	ACAATTTGTT	TTTGTTTCAGG	120
ATTAGGGATA	ACTGCATATA	CGCCATAGCG	AGCAATATAG	TCTGTATTCTG	CTTTTTTCTC	180
CGAAAGTTGG	GTTTGCCATT	GCATTTTCCT	CATTATCTAG	TATCGTTATT	ATTATAGTGA	240
AATGAACCAA	AAATAGTACA	CAATGTGGTA	TAATCTTTTT	ATGGCATATT	CAATAGATTT	300
TCGTAAAAAA	GTTCTCTCTT	ATTGTGAGCG	AACAGGTAGT	ATAACAGAAG	CATCACACGT	360
TTTCCAAATC	TCACGTAATA	CCATTTATGG	CTGGTTAAAG	CTAAAAGAGA	AAACAGGAGA	420
GCTAAACCAC	CAAGTAAAAG	GAACAAAACC	AAGAAAAGTT	GATAGAGATA	GACTTAAAAA	480
CTATCTTACT	GACAATCCAG	ACGCTTATTT	GACTGAAATA	GCTTCTGAAT	TTGGCTGTCA	540
TCCAACCTACC	ATCCACTATG	CACTCAAAGC	TATGGGCTAC	ACTCGAAAAA	AAGAACCACA	600

CCTACTATGA	ACAAGACCCA	GAAAAAGTAG	CCTTATTTCT	TAAGAATTTT	ANTAGTTTAA	660
AGCACCTAGC	ACAGGTCTAA	CAAATGGTGA	ATTAATCGCT	CCAATGACTT	ACGAAGAGAT	720
GATGACGAGC	GACTTTTGTG	AAGTATGGTT	TCAGAAGTTT	CTCTTACCAA	CATTAACCAC	780
ACCATCGGTT	ATTATAGTGA	AATGAAATAA	GAACAGGACN	AATCGATCAG	GACAGTAAAA	840
TCGAATTCTA	ACAATGTTTT	AGAAGTAGAG	GTGTACTATT	CTAGTTTCAA	TCTACTATAT	900
TAATGGACAA	TGCAAGATTC	CATAGAATGG	GTAAGCTAGA	GTTCTTATGT	GAAGAGTTTG	960
GGCATAAACT	TTTACCTTTT	CCTCCCTACT	CATCTTAGTA	TAGAAAAGTG	AATCTAAAAT	1020
AGTACATAAC	TGCTTCTAAA	ACATTCTTAT	AAATTGATTT	AAATTCTCAA	ATCATATTAT	1080
TCAGTTCTTA	TTTCATTTTG	CTCTACAATC	CTGTTGAGAA	GACACGTGTT	CATATCAAAA	1140
AGGTATTGGC	AAGTTGCAAT	ACCTTTTTTAC	AAGGTTCTTT	TGTCTTATTT	TTGTTTCAAC	1200
TGACTATATC	TCCTATGGTT	CTAGTTCAGA	AGGCTAGGCT	ATAATTATGA	TTGATAAGAA	1260
GTATCATTC	AAGTATTGAG	AGTGAATGTT	TCAAAATCAT	GGGTTTCTAT	AATGGTCAGG	1320
CTGGCATTTG	CTAGACCGCC	ATCTTTACGA	AGAAGTGGTT	CTTTATAGCC	TAGGAGAGTA	1380
CGAAGACTGG	CAGTAAGATT	GGCGCCGTGT	CCGACAATTA	GAATACGCTC	AGCTGGACTA	1440
TCTTTTAATG	ATTTGATAAA	TTGGATGGTC	CGCTGAGTTG	TACTATAGAG	GGATTCCGGCT	1500
CCGAACATTC	GAGTGTCAAA	TTGAGCAAGA	TTTGAACGAA	AAGCCTGGAT	TTGTTGCGGG	1560
TAAATAG						1567

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTGTTTCCAT	AGCATGACTT	CTGTACTAGA	CTTCTTTTTC	CGAATAAATA	GATAGAACCA	60
CAGAATCTAG	TAAACCTAGA	ATTAAAATTA	TGGTATAATA	TTAGCAATAA	AAGAAATCTG	120
GAGGATTAGA	ATCATGGTAT	CAACGAAAAC	ACAAATTGCT	GGTTTTGAGT	TTGACAATTG	180
CTTGATGAAT	GCAGCAGGTG	TGGCTTGTAT	GACGATAGAG	GAGTTAGAAG	AGGTCAAAAA	240
CTCAGCGGCA	GGAACCTTTG	TTACTAAGAC	AGCGACCTTG	GACTTCCGTC	AGGGGAATCC	300
TGAGCCACGC	TACCAAGATG	TTCCACTTGG	TTCCATCAAC	TCTATGGGCT	TGCCAAATAA	360
TGGCTTAGAC	TATTATTTGG	ATTATCTTTT	AGATTTGCAG	GAAAAAGAGT	CGAACCGAAC	420
TTTCTTCTTA	TCTCTGGTCG	GCATGTCTCC	AGAGAAACCC	ATACTATTTT	GAAAAAAGTC	480
CAGAGA						486

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

CTCTATCAGG AAAGTTAAAT TAATTTATAG AAATATTTTA GTATTTAAGC CCTACTGTTA      60
TAGATTCAAT AACTATATATA TGTGTTTGTC TGATAAAAAT TTCTACTCTT TTTGATTTTA      120
AATAAGTATT AGTTTACATT ATGGTGTGAA TTGGGTTTGA TATCTCTTTT GAGGAAGTTG      180
CCTTAGATTT TTCTGATTGT GTTTTATTGT ACAGTGATATC TTGCTTGTTT TGAACAGAAT      240
TTTTTATGAC ATTTGTCATA TTTTCTAGTG ACAGAAGCTT CTGCCCTCCTC TGATTTTAAA      300
AGACTATAAT TGTAAGTATGA AATGGGGGAA GAAGAGATGA GAAATAAAAT GATTATCGCA      360
GTAAGTTTAG TAGTAGCAGG AGTTATGACC TATCTCATGT TTTCCGGATT GGATGAGAAT      420
TTCTACCATT TTCCTTGGGA GGTCTTGCTT GGCTTTGGAA TCATCTTCTT GGCTTGTTCCA      480
GAGAAGGTTT GAAATTAGTA AGAGATGTGA AAAAGGAGTT TGAAAAATGA AAAAAGCAAC      540
TATCTATTTT TTTATCGGCC TGCACTCTT GGTATGGTTG GTAGAAATGT TTACAGGTTG      600
GTTTGCTCAA ACCTTCCTTC ACCAGTTCAT CCGTGGTGCA TGGGGATTAG GATTTATGAT      660
TTTTATCGCC TTTCCGATGG GAAAGGAGTT GCTGGAAGGA GAATATCATG AACATGATTA      720
AGGTTCAAGG ACTACATAAA AATATTAAGG GCAAGGCTAT TTCAAAGGAT ATTTCTTTTG      780
AAGTAGCAGA AGGTGAATGC GTTGCCTTGA TTGG                                     814

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(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

CTTGGTACGA CCGTATGGGT GGTCACTGAA AGTGGGAAAC TTCCAAGATG GGCAGTGTGT      60
ACGGATCCCC GTAAACTGTC GCANAAGAAC TGAAGATGAT GTTTTTACAG TTGTTTTCTT      120
CCATGGCTTT CAAAAGGCTG ACAGTTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA      180
TACGTGTTGA TTCGCCAACA GCCTTCAAAC CAGCAAAGTG AATGACACCA GTCAGTCTTT      240
CCTGCTTGAA AATATCTCTG AGGGTATCTG TGTCACNAAT ATCTGCCTCA TAGAAAGGAA      300
TCTCAACTCC TGTGATTCTT TCAACAACCT CTAACTCTT ACNATTGCTA TTGACAAGAT      360
TATCCACCAC AACAACTTGA TGGCCTGCTT GGATCAATTC AATAACAGTG TGGGTTCCAA      420
TAAACCCGGC ACCACCAGTT ACCAAAATCT TTTCTTGCAT CTTTTTTCCT CGATTCTCAG      480
ATTATTTTTT CTTATTTTAA CCATTTTGA CAGGGAATGT CATTTGCCAC CTAAACTAC      540

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CTGATAAAAT	TTCAGTAAAA	TGCTTATACT	CTTGAAAAAT	CCAATTCAAA	CCACGTCAAC	600
GTGCGCTTGC	CATGGGTATG	GTTACTGACT	TCGTCAAGTC	TATCCACAAC	CTCAAAGCAG	660
CGCTTTGAGT	AACCCGCGGC	TAGTTTCNTA	GTTTGTCTT	TGATTTTCAT	TGAGTATTAT	720
TCGCTTTTTA	CTCGTTTGAC	ATAGTTTTCA	ATTGGGTAGT	TTTCAGGGTC	CAAGGTCAAC	780
TCCTTGCTCT	GGATCAGTTG	AGCTAAATGG	TAACCAATAA	TAGGACCAGT	TGTGAGGCCT	840
GATGAACCTA	GTCCACTGGC	TGCATAGACA	CCAGTTAAGT	CAGGCACCTG	CCCAAAGAAA	900
GGAGAGAAAT	CACTGGTGTA	GGCACGGATT	CCAACACGCT	CAGATTTTGA	AGTAGCTTCA	960
GCCAAAATCA	GATAGTGAGT	CAAGGTGGCC	TCCTCCATTT	GTTGGAGCAA	GGTTTCATCT	1020
ACCGTCAAAT	CAAATCCCAT	GTCATTTTCG	TGGGTAGCGC	CTAAGGACAA	TTTCCCACCT	1080
GCAAAAGGAA	TCAAATCCCA	CTCCCCCTCT	GGCATGACAA	CAGGGTAAGC	TTCCATGTCT	1140
TGGACCAGCT	GATAATCTCG	TAGTTGTCTT	TTTTGAGGAC	GAACATCTAC	TTCATAACCC	1200
AAGGGTTCTA	ACATGTCCCC	CAACCAAGCT	CCNGTCGCCA	AAATAACCTG	CTCAAACCTC	1260
TCTTCACCAA	TCTGGTAGCC	TGATGCTAAC	GGTGTGAGAG	TCACTTTTTC	TTTGACCAG	1319

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAATAC	TGTTTTGAGG	TTGCAGATGG	AAGCTGACGC	GGTTTAAAGA	GATTTTCGAA	60
GAGTATAAAC	TGCTTATAAA	ATAAAAAGGA	GCCCTGATGG	AACACATTAT	TTATCAGTTT	120
GAAGAGGACT	TGGCAATCCT	TACCTTGAAC	CGTCCTGAGG	TCGCAAATGG	TTTTTCATATT	180
CCCATGTGTG	AGGAGATTTT	AGAAGCTCTG	ACTTTGGCAG	AAGAAAATCC	AGCTGTGCAT	240
TTTATCTTAA	TCAATGCCAA	TGGAAAGGTC	TTCTCAGTTG	GGGGAGATTT	GGTAGAGATG	300
AAGCGGGCAG	TGGATGAGGA	TGATATTCCA	TCATTGACAA	AAATCGCAGA	GTTGGTCAAT	360
ACGATTTCTT	ATAAAATCAA	GCAAATAGCC	AAACCTGTTT	TTAATGGAAG	TTGACGGTGC	420
TGTTGCAGGT	GCCGCAGCGA	ATATGGCTGT	TGCGGCAGAT	TTCTGTTTGG	CGACGGATAA	480
GGCTAAGTTT	ATCCCAAGCC	CTTTGTTGGT	GTGGTTGGCT	CCAGATTCCA	GGGG	534

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

CTGCAGCCGG AAGTTATCTG GTTACAAAAA ATCGCCAAAC CATCACAGAT GAAAGTCTTG      60
AATACCACTG ACCGCGTTCA AGCTATCAAG GACGATGTGG ATATTATCCA AAACAGCCTG      120
CAAATCATTA ACCAGCAAAA AGAAGTTATC AAGGAATACC AAGAAGACTT GACTTACAAG      180
TTTAAGGTCT TGGAAAAGGA TATCCAAACT AGGACTAGCT GTGATAAAAG AAATGCAGGG      240
AACTGAAGAT AAGTAAAAAG AGCCCGACGG CTCTTTTTTA AAACGTAAAC AAGTTATAGT      300
GAATTGAATT TAGAATAGCA CATCATAGTT TCTAAAGCAT TGTTAGAGAT TACTTTAAAA      360
TCCTCTTATC AATTTGTTC TATTCTATTT CAATCTACTA TATATATCCC ATCAACTATG      420
CATCATAATT TAGGTAATC ATACTCAATA AAAATCAAAA AGCAAACTAG AAAGCTAGGC      480
ACAGACTGCT CAAAACACCG TTTTAAGGTT GTGGATAGAA CTGACGAAGT CAGTAACCAT      540
ACCCATGACA AGCCGACGCT GACGTGGTTT GAAGAAATTT TTGAAGAGTA TCATTCACCA      600
TTTCACAACT AAATCGAAGA CTTTCTGCCG TAATGAAAAC ACCTGAAACA GCTTGGTTTC      660
AGCTGTCCGG AAAGTTTAAG ACTTAGGTTT AAAGTTTAGG TATGGAAGTT CGAAGGAGGT      720
CGCTACCGTC CGTCATTACT TAGNGAAGNC TTAATAAATC TATAAAGTAA AAAGAGCCCG      780
ACAG

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(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

CTACTCGTTT TAGTATAGTA AACTGAATCT AGACTAGCAC AATGCNGCTT CTANAGCGTT      60
TCGAAACTAG AATAGGACAA CATAACTGCT AAAAGATTTT TATAAATTCA TTTGATTTTC      120
CTAATCAATT TGTTTCGTAT CTANTTCACT CCACTATAAA ATATTCTTAT CAATTGATTT      180
GNATGCCAAA ATTCCATCGT TCAGGTCTTA TTTTATTNGG CTNTAAAAAA CTCTCCTGGG      240
NAATCCCAGG AGAGNATGAT TACNTATTTG AACTTGAATC CTTTCGTANAT AAGCTCTGTT      300
TTTGATTTT GTTTCCTAAT CTGTTTGCCA AGTGCCCTCA TCATAGAAAT AGGACCACAC      360
ATATAGACGG TTGCATGTTT GGGCACTTTT TTTGTTCAAA ATTAAGATAG CCGTCTTTTCG      420
TACTGTTCGAT TAGATGGAGT TCAAAATTAG GATTTTCTTG AGCATAGTTA CCGAGTAAAT      480
CTAGGTAGAC TGCATTTTCA TCTCCACGGA AGCTATAGTA GAAGTGAACC TGTATTATCTA      540
AAATAGGATG TTCACGGATG TAAGAGATGA AGGGGGTGAT CCCAATACCT CCAGCAATCC      600
AAACCTGATT TTCTCGTCCT TCTTCTATGA TCATGTGTCC GTAAGCTCTG TCTAGGGTTA      660
CTTTGCTGCC GGCTTGAAGA TTATCATAGA TATTTCTTGG TATGGTCGCC TGAATTTTAA      720
ACAGTAAAGT TAAAGAGTTT GAACCCATGA ACTCCCTGAG AATAGAAAAG GGATGCCCGA      780

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ACCACTTTCA	AAGCCTTCTT	GGAAAATCTT	TAGAAAGGCA	AATTGTCCTG	ATTGATAGTT	840
GAAAGGTCTG	CTAAGATGGA	TTTGAATTTC	TCTAGTATCG	TGATTTAAGC	GTTTGAGATG	900
GGTAATTTTC	CCTAGATAGG	GGAAGGAAAT	CTTTTGATAT	AGAAAAATGA	TATAAAAACC	960
AG						962

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CTCTTTCCAC	TATTATAACA	CGAAAGAAAG	AATTGTCAGG	GAACTGTACA	GATTTCTTTT	60
CTATCTATTT	ATAACTCAAT	GAAAATCAAA	GAGCAAAC TA	GGAAACTAGC	CGCAGGCTGT	120
AATTGAGTAC	GGCAAGGCGA	CGTTGACGCG	ATTTGAATTT	GATTTTCGCA	GAGTATTATT	180
CGTAAAAAAT	CTCAAAAAGC	CTACCTTTTCG	GTAGACTTAG	TTTGTTTCTA	TTCTAATCGG	240
CACTCTTCCA	AAATTTTGCT	CTGCTATACT	TGGCTTTCCT	AGTTGGTAAA	TCTGGTCAAC	300
CTTTTGAGTC	ATAGCATCCC	AAGGTTCTTT	GCCAATTCGG	CTGACTAGAT	TGACCTGTCC	360
TTTCAGAGAC	TTGAGATGTT	GCCTGCCTTT	TTCAGTAAAT	CCAAGGACAT	GAATGGCTTC	420
TGGCAAGTCA	CTTTCTCTAG	CCTGCATCAA	AATATAGGTC	AATAGGCGTC	TGACACGCGC	480
CTTGGTGTA	CGTTTGGTAG	TCACTAACTC	GACCAATTCT	TCCACAGACT	GGGCTGTTTT	540
AATAGCTTCT	TTAATGCGCA	CAGCCATTTT	TTGATTGACC	TGATAGATGG	TGGTTAGGTC	600
GGGATTTGAC	AAGATTTGAT	AGCGGAGCAA	GGGAAAATAG	TCTTCCCAGA	TCACCTTACT	660
GGCTTGCTCA	AATAGGGCAA	CAGAAGGCAT	AAAACGTTCT	AAGAAATCTT	GGTCCTTCTG	720
ATGTTGACGG	AGGGCTGTCT	CCGAGGCAAA	GTCCACATCT	TTATTCACAG	AATGGTAACC	780
TGCCCCCTGA	CGCTGAATCG	GATGCAGCTT	GATATTCCGT	CCTGCAACCG	CCTTGGCATA	840
GGCCAAAACA	AAGAACATGA	TTGGGGTGTA	TTACCTGAAA	AATCAAGACC	AGCAAATTCC	900
TTCCACATAG						910

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CGCCAAGTCA	TCCAACAAGT	CCAGAACGGT	TCTGGGGCTT	GGGATCCTCA	GTCGCTGGAG	60
ATAACTCCTT	TGGGCTTGTT	CATCATGTAG	TAGACAAACT	CTTCATACTC	CAACACTTGC	120
CCATCAAAAG	CGAATCTCAT	CTATTTTTC	ATCAATCTGC	AATTTAGCTG	ATTTTCTTT	180
TTTACCATTT	ACAGTCACGC	GCCCAGCCTT	GAGCAAGTTT	TTGACCTCAG	TCCGACTTCC	240
CACCGCACAG	GCAACTAAAA	ATTTATCTAA	TCTCATAGAA	CTATTATATC	ATATCAAAAG	300
GAGGCTGGTA	CAATGACCAA	CCTCCTTTTC	GTTTCATACT	CTTCAAAAAT	CTCTTCAAAC	360
CGCGTCAACG	TCGCCTTGCC	GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCTGCAACCT	420
CAAAGCAGTG	CTTTGAGCAA	CCTGCGGCTA	GTTTCCTAGT	TTGCTCTTTG	ATTTTCATTG	480
AGTATCAGAT	TTAGGAAATT	AACTTCCTCG	TCTCCAAAAA	ATAGCTAAGA	CAATCATGGC	540
ACCTAAAACA	GCTGGGATAA	TAGCTGTTC	TGATAAAACT	GGCCCCAAG	TTCCAAAGAG	600
CAAGTGACCT	AGAAAGGCTC	CGATCCAACC	GAGAAACATT	TTTCCAAAAC	ATCCCATTCG	660
CTCTCCACGA	TTGGTCATAG	CACCTGCTAA	AAATCCCACT	AGGAGACCAA	CGAACATACT	720
TCCTAACATA	TTATCTCCTT	AATTTGCCCA	ATTCCCATT	CGGAAAAGAA	GTACTCGCGT	780
TCCATCCTCA	CGAATACCAT	CGATATCCAT	TTGGTTAGAA	CCAATCATAA	AGTATACGTG	840
AACATCTGAA	CGGTTAAGCC	CTGCAG				866

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTTCAGGATG	TGGGAAAACG	ACCCTTCTTC	GTATGATTGC	AGGTTTCAAC	AGTATCAAAG	60
ATGGAGAATT	TTACTTCGAT	GATACAAAAA	TCAATAATAT	GGAACCCAGC	AAACGCAATA	120
TCGGGCTGGT	TTTCCAAAAC	TACGCTATTT	TCCCACATTT	GACTGTCCGA	GACAACGTTG	180
CTTTTGGTCT	TATGCAAAAG	AAGGTTCCAA	AAGAAGAATT	GATTCAACAG	ACCAACAAGT	240
ATCTTGGACT	CATGCAAATT	GCTCAATATG	CGGATCGAAA	GCCCGATAAA	CTCAGTGGTG	300
GACAACAACA	ACGTGTCACC	TTGGCATGCG	TCTTAGCGGT	TAATCCAAGT	GTTCTCCTCC	360
ATGGACGAAG	CCACTTAGTA	ATCTGGAGGC	CAAACCTTCGC	TTGGATATGC	GTTCAAGCCC	420
ATCCCGAGAA	ATCCAACCAC	GAAGTTGGGG	AATTACAAC	GTTTATGTAA	CCCACGACCA	480
AGAAGGAGCC	ATGGCTATTT	CAGACCAAAT	TGCCTGTTAT	GAAAGATGGG	GTGATCCAAC	540
AAATCGGCCG	ACCAAAAAGAA	CTGTATCATA	AACCAGCTAA	TGAGTTAGTG	GCAACCTTTA	600
TCGGACGCAC	AAATATTATC	CCTGCCAATC	TTGAAAAACG	GAGCGACGGC	GNTTATATCG	660
TCTNTTCAGA	TGGANANGCC	CTTCGAATGA	TAG			693

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Ser Met Phe Thr Met Val Lys Met Asn Pro Leu Arg Gly Leu Ile
 1           5           10           15
Cys Asn Leu Lys Gly Asn Lys Ile Thr Ala Leu Ile Gly Pro Ser Gly
      20           25           30
Ser Gly Lys Ser Thr Tyr Leu Arg Ser Leu Asn Arg Met Asn Asp Thr
      35           40           45
Ile Asp Ile Ala Lys Val Thr Gly Gln Ile Leu Tyr Arg Gly Ile Asp
      50           55           60
Val Asn Arg Pro Glu Ile Asn Val Tyr Glu Met Arg Lys His Ile Gly
      65           70           75           80
Met Val Phe Gln Arg Pro Asn Pro Phe Ala Lys Ser Ile Tyr Arg Asn
      85           90           95
Ile Thr Phe Ala His Glu Arg Ala Gly Val Lys Asp Lys Gln Val Leu
      100          105          110
Asp Glu Ile Val Glu Thr Ser Leu Ser Gln Ala Ala Leu Trp Asp Gln
      115          120          125
Val Lys Asp Asp Leu His Lys Ser Ala Leu Thr Leu Ser Gly Gly Gln
      130          135          140
Gln Gln Arg Leu Cys Ile Ala Arg Ala Ile Ser Val Lys Pro Asp Ile
      145          150          155          160
Leu Leu Met Asp Glu Pro Ser Leu Ser Leu Gly Ser Asp Cys Asp His
      165          170          175
Ala Thr Arg Arg Asp His Val
      180

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

Met Ile Lys Ile Ser Asn Leu Ser Lys Ser Phe Ser Gly Gln Thr Val
 1             5             10             15
Leu Asp His Leu Asn Leu Asp Ile Gln Lys Gly Glu Val Val Ala Leu
      20             25             30
Ile Gly Ser Ser Gly Ala Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn
      35             40             45
Tyr Leu Glu Thr Pro Asp Ser Gly Ser Ile Gln Ile Asp Gly Phe Ser
 50             55             60
Val Asp Phe Ser Lys Ile Thr Gln Glu Glu Ile Leu Ala Leu Arg Arg
65             70             75             80
Lys Leu Ser Met Val Phe Gln Gln Phe Asn Leu Phe Glu Arg Arg Thr
      85             90             95
Ala Leu Asp Asn Val Lys Glu Gly Leu Val Val Val Lys Lys Leu Ser
      100            105            110
Asp Gln Glu Ala Thr Lys Ile Ala Lys Glu Glu Leu Ala Lys Val Gly
      115            120            125
Leu Ser Asp Arg Glu Asn His Tyr Pro Arg His Leu Ser Gly Gly Gln
      130            135            140
Lys Gln Arg Val Ala Leu Ala Arg Ala Leu Ala Met Lys Pro Asp Val
      145            150            155            160
Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu Val Gly
      165            170            175
Glu Val Glu Lys Ser Ile Ala Asp Ala Ala Lys Ser Gly Gln Thr Met
      180            185            190
Ile Leu Val Ser His Asp Met Pro Phe Val Ala Gln Val Ala Asp Lys
      195            200            205
Ile Leu Phe Leu Asp Lys Gly Lys Ile Ile Glu Ser Gly Thr Pro Asp
      210            215            220
Glu Ile Ile His Thr Pro Lys Glu Glu Arg Thr Lys Glu Phe Phe Thr
      225            230            235            240
Ser Tyr Lys Arg Thr Tyr Ile
      245

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Phe Ser Leu Arg Ser Val Phe Asp Gly Ile Pro Arg Ile Val Gln
 1           5           10           15
Gln Leu Pro Thr Thr Ile Met Leu Thr Ile Gly Gly Ala Leu Phe Gly
      20           25           30
Leu Val Leu Ala Leu Leu Phe Ala Ile Val Lys Ile Asn Arg Val Lys
      35           40           45
Ile Leu Tyr Pro Leu Gln Ala Phe Phe Val Ser Phe Leu Lys Gly Thr
      50           55           60
Pro Ile Leu Val Gln Leu Met Leu Thr Tyr Tyr Gly Ile Pro Leu Ala
65           70           75           80
Leu Lys Ala Leu Asn Gln Gln Trp Gly Thr Gly Leu Asn Ile Asn Ala
      85           90           95
Ile Pro Ala Ala Ala Phe Ala Ile Val Ala Phe Ala Phe Asn Glu Ala
      100          105          110
Ala Tyr Ala Ser Glu Thr Ile Arg Ala Ala Ile Leu Ser Val Asn Pro
      115          120          125
Gly Glu Ile Glu Ala Ala Arg Ser Leu Gly Met Thr Arg Ala Gln Val
      130          135          140
Tyr Arg Arg Val Ile Ile Pro Asn Ala Ala Val Val Ala Thr Pro Thr
145          150          155          160
Leu Ile Asn Ser Leu Ile Gly Leu Thr Lys Gly Thr Ser Leu Ala Phe
      165          170          175
Ser Ala Gly Val Val Glu Val Phe Ala Gln Ala Gln Ile Leu Gly Gly
      180          185          190
Ala Asp Tyr Arg Tyr Phe Glu Arg Phe Ile Ser Val Ala Leu Val Tyr
      195          200          205
Trp Val Val Asn Ile Gly Ile Glu Ser Leu Gly Arg Phe Ile Glu Arg
      210          215          220
Lys Met Ala Ile Ser Ala Pro Asp Thr Val Gln Thr Asp Val Lys Gly
225          230          235          240
Asp Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Met Tyr Arg Ile Asp Asp Asp Glu Gln Phe Val Leu Asp Phe Leu Lys
 1             5             10             15
Gln Glu Lys Val Leu Leu Val His Gly Arg Gly Phe Asn Trp Gln Glu
      20             25             30
Pro Asp His Phe Arg Ile Val Tyr Leu Pro Arg Val Asp Glu Leu Ala
      35             40             45
Gln Ile Gln Glu Lys Met Thr Arg Phe Leu Lys Gln Tyr Arg Arg
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Met Asn Asp Glu Ala Ser Lys Gln Leu Thr Asp Ala Arg Phe Lys Arg
 1             5             10             15
Leu Val Gly Val Gln Arg Thr Thr Phe Glu Glu Ile Leu Ala Val Leu
      20             25             30
Lys Thr Ala Tyr Gln Leu Lys His Ala Lys Gly Gly Arg Lys Pro Lys
      35             40             45
Leu Ser Leu Glu Asp Leu Leu Met Ala Thr Leu Gln Tyr Val Arg Glu
 50             55             60
Tyr Arg Thr Tyr Glu Gln Ile Ala Ala Asp Phe Gly Ile His Glu Ser
 65             70             75             80
Asn Leu Ile Arg Arg Ser Gln Trp Val Glu Val Thr Leu Val Gln Ser
      85             90             95
Gly Val Thr Ile Ser Arg Thr Pro Leu Ser Ser Glu Asp Thr Val Met
      100             105             110
Ile Asp Ala Thr Glu Val Gln Ile Asn Arg Pro Lys Lys Arg Ile Ser
      115             120             125

```

Glu Ser Phe Trp
130

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met	Arg	Arg	Lys	Tyr	Lys	Ser	Ile	Ala	Leu	Lys	Lys	Glu	Leu	Ala	Asn
1			5						10					15	
His	Ser	Gly	Lys	Lys	Lys	Phe	His	Ala	Met	Lys	Ala	Gln	Ala	Ile	Val
			20					25					30		
Thr	Ser	Gln	Gly	Arg	Ile	Val	Ser	Leu	Asp	Ile	Ala	Val	Asn	Tyr	Ser
			35					40				45			
His	Asp	Met	Lys	Leu	Phe	Lys	Met	Ser	Cys	Arg	Asn	Ile	Gly	Gln	Ala
			50				55				60				
Gly	Lys	Ile	Leu	Ala	Asp	Ser	Gly	Tyr	Gln	Gly	Pro	Met	Lys	Ile	Tyr
65					70				75					80	
Pro	Gln	Ala	Gln	Thr	Pro	Arg	Lys	Ser	Ser	Lys	Leu	Lys	Pro	Leu	Ile
			85					90					95		
Ala	Glu	Asp	Lys	Ala	Tyr	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys
			100					105					110		
Val	Glu	Asn	Ile	Phe	Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr
			115				120				125				
Thr	Tyr	Arg	Asn	His	Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu	Ile
			130				135				140				
Ala	Gly	Ile	Ile	Asn	Tyr	Glu	Leu	Gly	Phe						
145							150								

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Met Val Ser Ser Ser Gly Ser Glu Phe Gln Ser Gly Trp Gln Glu His
 1             5             10             15
Gln Leu Ile Ala Glu Lys Val Ser Lys Thr Leu Asp Lys Thr Phe Asp
          20             25             30
Lys Asp Val Arg Lys Ile Pro Thr Ser Pro Val Leu Ser Lys Ile Cys
          35             40             45
Arg

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
 1             5             10             15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
          20             25             30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
          35             40             45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
          50             55             60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
          65             70             75             80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
          85             90             95
Gln Asn Met Val
          100

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Met Asn Thr Lys Met Met Ser Gln Phe Ser Val Met Asp Asn Glu Met
 1             5             10             15
Leu Ala Cys Val Glu Gly Gly Asp Ile Asp Trp Gly Arg Glu Ile Ser
          20             25             30
Cys Ala Ala Gly Val Ala Tyr Gly Ala Ile Asp Gly Cys Ala Thr Thr
          35             40             45
Val

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Met Arg Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
 1             5             10             15
Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
          20             25             30
Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
          35             40             45
Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
          50             55             60
Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
          65             70             75

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Met Ala His Gly Asp Leu Leu Tyr His Asp Gly Leu Phe Phe Ser Ala
 1             5             10             15
Lys Lys Glu Asp Gly Thr Tyr Asp Phe His Glu Asn Phe Glu Tyr Val
          20             25             30
Thr Pro Trp Leu Lys Gln Val Asp
      35             40

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Met Ser Leu Ile Thr His Arg Arg Phe Ile Ser Cys Asn Glu Asn Ile
 1             5             10             15
Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Lys Cys Val Asn Asp
          20             25             30
Leu Met Ala Glu Leu Asn Ser Val Ile Thr Thr Val Thr Gly Ile Glu
      35             40             45
Asn Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala
      50             55             60
Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser
65             70             75             80
Ile Tyr Gln Ser Gly Gln Ile Asp Leu Val Gly Arg Met Val Lys Arg
          85             90             95
Gly Ser Leu His Leu Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Ile Arg Ala Val Phe Phe Ser Ile Asp Asn Asp Met Glu Glu Ala
 1             5             10             15
Ala Arg Ser Met Gly Ala Ser Ser Phe Tyr Thr Met Val Arg Val Ile
      20             25             30
Ile Pro Tyr Ile Leu Pro Val Val Leu Ser Val Val Val Leu Asn Phe
      35             40             45
Asn Ser Leu Leu Ser Asp Tyr Asp Leu Ser Val Phe Leu Tyr His Pro
      50             55             60
Leu Phe Gln Pro Leu Gly Ile Val Ile Lys Gln Ser Thr Asp Glu Thr
      65             70             75             80
Ala Thr Leu Asn Ala Gln Ala Met Met Phe Val Tyr Ser Val Ile Leu
      85             90             95
Met Ile Met Ser Ser Ala Ala Leu Tyr Leu Ser Ser Leu Phe Gln Gly
      100             105             110
Lys Arg Gly Lys Arg
      115

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile Pro Ala Ser
 1             5             10             15
Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe Asn Ser Glu
      20             25             30

```


Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln Val Gln
 35 40 45
 Thr Met Leu Glu Gln Ala Phe Thr Glu Lys His Tyr Glu Asn Thr Ile
 50 55 60
 Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His Arg
 65 70 75 80
 Phe Leu Arg Val Arg Glu Phe Lys His Leu Cys His Ala Arg Glu Thr
 85 90 95
 Ala Lys Thr Thr Val
 100

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Glu Ile Leu Thr Thr Gln Gln Val Arg Glu Gly Tyr Gln Ala Ile
 1 5 10 15
 Leu Ala Ser Pro Leu Gly Leu Gln Asp Ala Phe Glu Val Ala Gln Glu
 20 25 30
 Lys Ser Gly Ser Tyr Thr Val Pro Pro Glu Ile Asp Gly Trp Lys Gly
 35 40 45
 Asn Thr Glu Pro Leu Arg Ile Asp Tyr Val Phe Thr Thr Lys Glu Leu
 50 55 60
 Ala Val Glu Asn Leu His Val Val Phe Asp Gly Asn Lys Ser Pro Gln
 65 70 75 80
 Val Ser Asp His Tyr Gly Leu Asn Ala Met Leu Asn Trp Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

Met Leu Lys His Leu Asn Leu Lys Gly His Leu Leu Thr Ala Ile Ser
 1             5             10             15
Tyr Met Ile Pro Ile Val Cys Gly Ala Gly Phe Leu Val Ala Ile Gly
      20             25             30
Leu Ala Met Gly Gly Gly Val Pro Asp Ala Leu Val Ala Gly Lys Phe
      35             40             45
Thr Ile Trp Asp Ala Leu Ala Thr Met Gly Gly Lys Ala Leu Gly Leu
      50             55             60
Leu Pro Val Val Ile Ala Thr Gly Leu Ser Tyr Ser Ile Ala Gly Lys
65             70             75             80
Pro Gly Ile Ala Pro Gly Phe Val Val Gly Leu Ile Ala Asn Ser Val
      85             90             95
Gly Ser Gly Phe Ile Gly Gly Ile Leu Gly Gly Tyr Ile Val Gly Phe
      100            105            110
Leu Val Gln Ala Ile Ile Lys Lys Val Lys Val Pro Asn Trp Ile Lys
      115            120            125
Gly Leu Met Pro Thr Leu Ile Ile Pro Phe Val Pro Leu Trp
      130            135            140

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
 1             5             10             15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
      20             25             30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
      35             40             45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
      50             55             60

```

Val Gly Leu Val His Thr Ala Asp Ala Ala Lys Lys Gly Asp Phe
 65 70 75 80
 Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
 85 90 95
 Arg Ile Ala Leu Pro Ala Ala Leu Leu Leu Met Val Pro Thr Glu Thr
 100 105 110
 Val Gln Ser Ile Leu Ser Ala Met Pro Asp Trp Leu Lys Asp Gly Met
 115 120 125
 Ala Ile Gly Gly Gly Met Val Val Ala Val Gly Tyr Ala Met Val Ile
 130 135 140
 Asn Met Met Ala Thr Arg Glu Val Trp Pro Phe Phe Ala Leu Gly Phe
 145 150 155 160
 Val Leu Ala Ala Val Ser Asp Ile Thr Leu Ile Gly Phe Gly Ala Ile
 165 170 175
 Gly Val Ala Ile Ala Leu Ile Tyr Leu His Leu Ser Lys Thr Gly Gly
 180 185 190
 Asn Gly Gly Gly Gly Ala Ala Thr Ser Asn Asp Pro Ile Gly Asp Ile
 195 200 205
 Leu Glu Asp Tyr
 210

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
 1 5 10 15
 Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
 20 25 30
 Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
 35 40 45
 Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
 50 55 60
 Thr Ala Ser Leu
 65

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

Met Thr Lys Leu Leu Asn Lys Lys Trp Lys Val Lys Ile Met Lys Gln
 1             5             10             15
Ile Leu Leu Val Cys Asn Ala Gly Met Ser Thr Ser Met Leu Val Lys
      20             25             30
Lys Met Gln Gln Ser Ala Thr Glu Arg Gly Ile Glu Ile Ser Ile Gln
      35             40             45
Ala Lys Ser Met Thr Glu Ala Lys Lys Asn Ile His Glu Ala Asp Val
      50             55             60
Ile Leu Ile Gly Pro Gln Ile Arg Tyr Glu Leu Leu Ala Val Lys Glu
65             70             75             80
Ile Ala Gly Asn Ile Pro Val Asp Thr Ile Asp Met Arg Asp Tyr Gly
      85             90             95
Met Met Asn Gly Ala Lys Val Leu Glu Gln Ala Leu Glu Trp Ile Gly
      100            105            110
Glu Ile Arg
      115

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

Met Val Leu Met Gln Lys Met His Gly Lys Glu Leu Ile Thr Leu Asn
 1             5             10             15

```

Gln Thr Val Lys Trp Tyr Lys Val Ser Gly Phe Met Ile Leu Leu Thr
 20 25 30
 Lys Pro Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Arg Asn Ala
 35 40 45
 Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn
 50 55 60
 Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr Tyr Leu Thr Ser
 65 70 75 80
 Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Pro Lys
 85 90 95
 Ile Gly Trp

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Leu Thr Val His Gly Lys Glu Ile Thr Ile Leu Lys Ser Asp Gly
 1 5 10 15
 Lys Met Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly
 20 25 30
 Ala Asp Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Ala Ser Pro Ser
 35 40 45
 Asn Asp Ser Asn Ser Glu Tyr Ser Cys Cys Phe Arg Lys Gly Lys Lys
 50 55 60
 Leu
 65

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Leu Phe Asn
 1           5           10           15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Tyr
      20           25           30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
      35           40           45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
      50           55           60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
65           70           75           80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
      85           90           95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
      100          105          110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
      115          120          125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
      130          135          140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
      145          150          155          160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
      165          170          175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
      180          185          190
Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Cys Gly Asp Ser Gly
      195          200          205
Ser Lys Gly Leu Ala Asp Ile Leu Ser Gln Ser Ile Ser Leu Val Glu
      210          215          220
Asn
225

```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Met Thr Ile Phe Pro Asp Asp Phe Leu Trp Gly Gly Ala Val Ala Ala
 1           5           10           15
Asn Gln Val Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val
          20           25           30
Gln Asp Val Leu Pro Lys Gly Gly Leu Gly Glu Ala Thr Glu Asn Pro
          35           40           45
Thr Glu Asp Asn Leu Lys Leu Ile Gly Ile Asp Phe Tyr His Lys Tyr
          50           55           60
Lys Glu Asp Ile Ser Leu Phe Ser Glu Met Gly Phe Asn Val Phe Arg
65           70           75           80
Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Lys Gly Asp Glu Glu Glu
          85           90           95
Pro Asn Glu Ala Gly Leu Lys Tyr Tyr Asp Glu Leu Phe Asp Glu Leu
          100          105          110
His Ala His Gly Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr
          115          120          125
Pro Leu Tyr Leu Ala Arg Lys Tyr His Gly Trp Ile Asp Arg Lys Asn
          130          135          140
Asp Ser Phe Leu
145

```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

Met Ile Glu Tyr Lys Asn Val Ala Leu Arg Tyr Thr Glu Lys Asp Val
 1           5           10           15
Leu Arg Asp Val Asn Leu Gln Ile Glu Asp Gly Glu Phe Met Val Leu
          20           25           30
Val Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Lys Met Ile Asn
          35           40           45
Arg Leu Leu Glu Pro Thr Asp Gly Asn Ile Tyr Met Asp Gly Lys Arg
          50           55           60

```

```

Ile Lys Asp Tyr Asp Glu Arg Glu Leu Arg Leu Ser Thr Gly Tyr Val
65          70          75          80
Leu Gln Ala Ile Ala Leu Phe Pro Asn Leu Thr Val Ala Glu Asn Ile
          85          90          95
Ala Leu Ile Pro Glu Met Lys Gly Trp Ser Lys Glu Glu Ile Thr Lys
          100         105         110
Lys Thr Glu Glu Leu Leu Ala Lys Val Gly Leu Pro Val Ala Glu Tyr
          115         120         125
Gly His Arg Leu Pro Ser Glu Leu Ser Gly Gly Glu Gln Gln Arg Val
          130         135         140
Gly Ile Val Arg Ala Met Ile Gly Gln Pro Lys Ile Phe Leu Met Asp
145          150          155          160
Glu Pro Phe Ser Ala Leu Asp Ala Ile Ser Arg Lys Gln Leu Gln Val
          165         170         175
Leu Thr Lys Glu Leu His Lys Glu Phe Gly Met Thr Thr Ile Phe Val
          180         185         190
Thr His Asp Thr Asp Glu Ala Leu Lys Leu Ala Asp Arg Ile Ala Val
          195         200         205
Leu Gln Asp Gly Glu Ile Arg Gln Val Ala Asn Pro Glu Thr Ile Leu
          210         215         220
Lys Val Pro Ala Thr Asp Phe Val Ala Asp Leu Phe Gly Gly Ser Val
225          230          235          240
His Asp

```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Met Pro Phe Val Pro Gly Ile Ala Leu Thr Asn Ala Val Arg Asp Ile
1          5          10          15
Met Thr Asn His Ile Asn Ser Gly Met Ser Lys Met Phe Glu Ser Leu
          20          25          30
Leu Ile Thr Leu Ala Leu Gly Ala Gly Thr Ser Val Ala Leu Val Leu
          35          40          45

```


Met Asn

50

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Tyr Thr Ile Arg Met Leu Lys Met Gly Ser Glu Ala Ala Ala Lys
 1             5             10             15
Ser Ala Gln Glu His Gly Leu Lys Ser Val Glu Val Thr Val Lys Gly
          20             25             30
Pro Gly Ser Gly Arg Glu Ser Ala Ile Ser Cys Ala Cys Cys Arg Trp
          35             40             45
Ser

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Ile Glu Phe Glu Lys Pro Asn Ile Thr Lys Ile Asp Glu Asn Lys
 1             5             10             15
Asp Tyr Gly Lys Leu Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
          20             25             30
Ala Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ala Ser Leu Pro Gly
          35             40             45
Ala Ala Val Thr Ser Ile Asn Ile Asp Gly Val Leu His Glu Phe Asp
          50             55             60

```

```

Thr Val Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Ile
65          70          75          80
Lys Gly Ile Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
          85          90          95
Leu Asp Val Glu Gly Pro Ala Glu Val Thr Ala Gly Asp Ile Leu Thr
          100         105         110
Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
          115         120         125
Gly Glu Gly Ser Ser Leu Lys Ala Thr Met Thr Val Asn Ser Gly Arg
          130         135         140
Gly Tyr Val Pro Ala Asp Glu Asn Lys Lys Asp Asn Ala Pro Val Gly
145          150          155          160
Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Thr Lys Val Asn Tyr
          165         170         175
Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
          180         185         190
Thr Leu Glu Ile Leu Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
          195         200         205
Gly Leu Ser Ala Arg Ile Leu Thr Glu His Leu Asp Leu Phe Thr Asn
          210         215         220
Leu Thr Glu Ile Ala Lys Ser Thr Glu Val Met Lys Glu Ala Asp Thr
225          230         235         240
Glu Ser Asp Asp Arg Ile Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
          245         250         255
Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
          260         265         270
His Asp Leu Thr Glu Lys Ser Glu Ala Glu Met Met Lys Val Arg Asn
          275         280         285
Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Leu Lys Leu Ile Asp Leu
          290         295         300
Gly Leu Gly Leu Lys Asp Lys
305          310

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Met Asp Ile Glu Lys Gln Arg Gly Ile Ser Val Thr Ser Ser Val Met
 1              5              10              15
Gln Phe Asp Tyr Asp Gly Lys Arg Val Asn Ile Leu Asp Thr Pro Gly
      20              25              30
His Glu Asp Phe Ser Glu Asp Thr Tyr Arg Thr Leu Met Ala Val Asp
      35              40              45
Ala Ala Val Met Val Val Asp Ser Ala Lys Gly Ile Glu Ala Gln Thr
      50              55              60
Lys Lys Leu Phe Glu Val Val Lys His Arg Gly Ile Pro Val Phe Thr
      65              70              75              80
Phe Met Asn Lys Leu Asp Arg Asp Gly Arg Glu Pro Leu Asp Leu Leu
      85              90              95
Gln Glu Leu Glu Glu Ile Leu Gly Ile Ala Ser Tyr Pro Met Asn Trp
      100             105             110
Pro Ile Gly Met Gly Lys Ala Phe Glu Gly Leu Tyr Asp Leu Tyr Asn
      115             120             125
Gln Arg Leu Glu Leu Tyr Lys Gly Asp Glu Arg Phe Ala Ser Pro Arg
      130             135             140
Arg Trp Arg Gln Thr Phe Trp
145             150

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ala Val Ile Ala Glu Arg Lys Ala Tyr Tyr His Asp Pro Val Glu
 1              5              10              15
Asp Ala Ile Ile Met Lys Arg Glu Ile Asp Glu Gly
      20              25

```

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```

Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys His Gly
 1              5              10              15
Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly
          20              25              30
Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser
          35              40              45
Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys
          50              55              60
Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly
65              70              75              80
Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser
          85              90              95
Val Ile Pro His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val
          100             105             110
Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln
          115             120             125
Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu
          130             135             140
Tyr Gln Asn Gly Phe
145

```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Met Asn Trp Ser Ala Leu Glu Gln Gln Ile Val Asp Glu Leu Lys Ile
 1              5              10              15
Tyr Ile Ala Pro Lys Ile Phe Gly Gly Ser Ala Lys Phe Pro Val Gly
          20              25              30

```

Gly Glu Gly Ile Ser Leu Pro Asn Asp Ala Ile Arg Leu Lys Pro Tyr
 35 40 45
 Ala Phe Ser Gln Xaa Gly Xaa Asp Tyr Leu Ile Glu Ser Glu Val Ile
 50 55 60
 Tyr Pro Cys Ser Gln Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Val Leu Phe Leu Val Pro Gln Leu Arg Asn Ala Tyr Gly Thr Ala
 1 5 10 15
 Ala Ile Gly Ile Ile Cys Gly Leu Tyr Trp Ala Val Ser Ser Asn Met
 20 25 30
 Thr Val Glu Ala Thr Gln Arg Leu Thr Gly Gly Gly Gly Phe Ala Ile
 35 40 45
 Gly His Gln Gln Gln Phe Ala Ile Trp Phe Val Asp Lys Val Ala Gly
 50 55 60
 Arg Phe Gly Lys Lys Glu Glu Ser Leu Asp Asn Leu Lys Leu Pro Lys
 65 70 75 80
 Phe Leu Ser Ile Phe His Asp Thr Val Val Ala Ser Ala Thr Phe Asp
 85 90 95
 Ala Arg Ile Leu Arg Gly His Ser Phe Asn Leu Gly Ser Arg His Tyr
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
 1           5           10           15
Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
          20           25           30
Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
          35           40           45
Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
          50           55           60
Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
65           70           75           80
Gly Lys Ser Ser Leu Val Gln Leu Leu Leu Gly Leu Tyr Pro Val Asp
          85           90           95
Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
          100          105          110
Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
          115          120          125
Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
          130          135          140
Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
          145          150          155          160
Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
          165          170          175
Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
          180          185          190
Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
          195          200          205
Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
          210          215          220
Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
          225          230          235          240
Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Leu Glu Lys Gly Glu Leu
          245          250          255
Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
          260          265          270
Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
          275          280

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

Met Lys Asp Pro Glu Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln
 1             5             10             15
Val Ile Gly Thr Cys Thr Val Asp Leu Ser Thr Asn Thr Asn Tyr Phe
          20             25             30
Tyr Gly Leu Ala Ile Leu Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser
          35             40             45
Tyr Leu Ala Lys Ser Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys
          50             55             60
Glu Phe Gln Ile Ala Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu
65             70             75             80
Tyr Glu Lys Ile Gly Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn
          85             90             95
Glu Lys Gly Ala Arg Asp Ser Glu Val
          100             105

```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Met Phe Ala Leu Ser Ser Asn Lys Glu Leu Ala Glu Arg Val Ala Gln
 1             5             10             15
Glu Ile Gly Ile Glu Leu Gly Lys Ser Ser Val Arg Gln Phe Ser Asp
          20             25             30
Gly Glu Ile Gln Val Asn Ile Glu Ser Ile Arg Gly Lys His Val
          35             40             45
Phe Ile Leu Gln Ser Thr Ser Ser Pro Val Asn Asp Asn Leu Leu Glu
50             55             60

```

```

Ile Leu Ile Met Val Asp Ala Leu Lys Arg Ala Ser Ala Glu Ser Val
65          70          75          80
Asn Val Val Met Pro Tyr Tyr Gly Tyr Ala Arg Gln Asp Arg Lys Ala
          85          90          95
Arg Ala Arg Glu Pro Ile Thr Ser Lys Leu Val Ala Asn Met Leu Glu
100        105        110
Val Ala Gly Val Asp Arg Leu Leu Thr Ile Asp Leu His Ala Ala Gln
115        120        125
Ile Gln Gly Phe Phe Asp Ile Pro Val Asp His Leu Met Gly Ala Pro
130        135        140
Leu Ile Ala Asp Tyr Phe Glu Arg Pro Gly Met Val Gly Ser Asp Tyr
145        150        155        160
Val Val Val Ser Pro Asp His Gly Gly Val Thr Arg Ala Arg Lys Leu
165        170        175
Ala Glu Phe Leu Lys Thr Ser Ile Ala Ile Ile Glu Lys Arg Arg Ser
180        185        190
Val Asp Lys Met Asn Thr Ser Glu Val Met Asn Thr Ile Gly Lys Val
195        200        205
Glu Gly Asn His Leu
210

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Met Ile Ser Phe Leu Leu Leu Leu Val Leu Val Trp Gly Phe Tyr Ile
1          5          10          15
Gly Tyr Arg Arg Gly Leu Leu Leu Gln Val Tyr Tyr Leu Ile Ser Ala
20        25        30
Met Ala Ser Ala Phe Met Ala Gly Gln Phe Tyr Lys Gly Leu Gly Glu
35        40        45
Gln Phe His Leu Leu Leu Pro Tyr Ala Asn Ser Gln Glu Gly Gln Gly
50        55        60
Thr Phe Phe Phe Pro Ser Asp Gln Leu Phe Gln Leu Asp Lys Val Phe
65        70        75        80

```


Tyr Ala Gly Ile Gly Tyr Leu Leu Val Phe Gly Ile Val Tyr Ser Ile
 85 90 95
 Gly Arg Leu Leu Gly Leu Leu Leu His Leu Ile Pro Ser Lys Lys Leu
 100 105 110
 Gly Gly Lys Leu Phe Gln Val Ser Ala Gly Ile Leu Ser Met Leu Val
 115 120 125
 Thr Leu Phe Val Leu Gln Met Ala Leu Thr Ile Leu Ala Thr Ile Pro
 130 135 140
 Met Ala Val Ile Gln Asn Pro Leu Glu Lys Ser Ile Val Ala Lys His
 145 150 155 160
 Ile Ile Gln Ser Ile Pro Ile Thr Thr Ser Trp Leu Lys Gln Ile Trp
 165 170 175
 Val Thr Asn Leu Ile Gly
 180

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met Arg Ala Phe Ser Asp Phe Gly Thr Pro Met Leu Ile Gly Glu Gly
 1 5 10 15
 Tyr Arg Thr Phe Pro Val Leu Ile Tyr Thr Gln Phe Ile Ser Glu Val
 20 25 30
 Gly Gly Asn Ser Ala Phe Ala Ile Met Ala Ile Ile Ile Ala Leu Ala
 35 40 45
 Ile Phe Leu Ile Gln Lys His Ile Ala Asn Arg Tyr Ser Phe Ser Met
 50 55 60
 Asn Leu Leu His Pro Ile Glu Pro Lys Lys Thr Thr Lys Gly Lys Met
 65 70 75 80
 Ala Ala Ile Tyr Ala Thr Val Tyr Gly Ile Ile Phe Ile Ser Val Leu
 85 90 95
 Pro Gln Ile Tyr Leu Ile Tyr Thr Ser Phe Leu Lys Thr Ser Gly Met
 100 105 110
 Val Phe Val Lys Gly Tyr Ser Pro Asn Ser Tyr Lys Val Ala Phe Asn
 115 120 125

Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala
 130 135 140
 Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Val Pro Tyr Ile Val Pro Gly Thr Val Leu Gly Ile Ala Phe Ile
 1 5 10 15
 Ser Ser Phe Asn Thr Gly Leu Phe Gly Ser Gly Phe Leu Met Ile Thr
 20 25 30
 Gly Thr Ala Phe Ile Leu Ile Met Ser Leu Ser Val Arg Arg Leu Pro
 35 40 45
 Tyr Thr Ile Arg Ser Ser Val Ala Ser Leu Gln Gln Ile Ala Pro Ser
 50 55 60
 Ile Glu Glu Ala Ala Gly Lys Leu Arg Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Phe Ile Pro Met Ala Ala Tyr Ser Ile Ala Arg Asn Met Ser
 1 5 10 15
 Lys Arg Lys Ala Phe Thr Ile His Val Tyr Pro Leu Asn Pro Arg Asn
 20 25 30

Leu Arg Thr Phe Pro Ser His His Asp Ser Asp Tyr Gly Tyr Asp Glu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
 1 5 10 15
 Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
 20 25 30
 Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
 35 40 45
 Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
 50 55 60
 Lys Ser Ile Ile Gln Ala Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Asn Ser Gln Gln Lys Pro Gln Glu Ile Lys Val Glu Glu Pro Val
 1 5 10 15
 Glu Ser Lys Glu Glu Thr Val Asn Gln Pro Val Glu Gln Pro Lys Val
 20 25 30
 Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
 35 40 45

```

Val Glu Val Thr Ser Ile Pro Gln Thr Thr Arg Tyr Glu Glu Asp Leu
   50                      55                      60
Thr Lys Glu His Gly Thr Arg Glu Val Val Lys Glu Gly Lys Asn Gly
  65                      70                      75                      80
Ser Arg Thr Val Thr Thr Pro Tyr Ile Leu Asn Ala Thr Asp Gly Thr
                      85                      90                      95
Thr Thr Glu Gly Thr Ser Thr Thr Asp Glu Ala Glu Met Glu Lys Glu
                      100                      105                      110
Val Val Arg Val Gly Thr Lys Pro Lys Glu Lys Leu Ala Pro Val Leu
                      115                      120                      125
Ser Leu Thr Ser Val Thr Asp Asn Ala Met Leu Arg Ser Ala Arg Leu
                      130                      135                      140
Thr Tyr His Leu Glu Asn Thr Asp Ser Val Asp Val Lys Lys Ile His
  145                      150                      155                      160
Ala Glu Ile Lys Asn Gly Asp Lys Val Val Lys Thr Ile Asp Leu Ser
                      165                      170                      175
Lys Glu Arg Leu Ser Asp Ala Val Asp Gly Leu Glu Leu Tyr Lys Asp
                      180                      185                      190
Tyr Lys Ile Val Thr Ser Met Thr Tyr Asp Arg Gly Asn Gly Glu Glu
                      195                      200                      205
Thr Ser Thr Leu Glu Glu Thr Pro Leu Arg Leu Asp Leu Lys Lys Val
                      210                      215                      220
Glu Leu Lys Asn Ile Gly Ser Thr Asn Leu Val Lys Val Asn Glu Asp
  225                      230                      235                      240
Gly Thr Glu Val Ala Ser Asp Phe Leu Thr Ser Lys Pro Val Asp Val
                      245                      250                      255
Gln Asn Tyr Tyr Leu Lys Val Thr Ser Arg Asp Asn Lys Val Val Ser
                      260                      265                      270
Pro Pro Ser
                      275

```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

Met Ala Val Met Lys Ile Glu Tyr Tyr Ser Gln Val Leu Asp Met Glu
 1              5              10              15
Trp Gly Val Asn Val Leu Tyr Pro Asp Ala Asn Arg Val Glu Glu Pro
      20              25              30
Glu Cys Glu Asp Ile Pro Val Leu Tyr Leu Leu His Gly Met Ser Gly
      35              40              45
Asn His Asn Ser Trp Leu Lys Arg Thr Asn Val Glu Arg Leu Leu Arg
      50              55              60
Gly Thr Asn Leu Ile Val Val Met Pro Asn Thr Ser Asn Gly Trp Tyr
      65              70              75              80
Thr Asp Thr Gln Tyr Gly Phe Asp Tyr Tyr Thr Ala Leu Ala Glu Glu
      85              90              95
Leu Pro Gln Val Pro Glu Thr Leu Leu Pro
      100              105

```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```

Met Arg Leu Leu Ala Met Lys Met Lys Gln Ile Ser Asp Thr Thr Leu
 1              5              10              15
Lys Ile Thr Met Ser Leu Glu Asp Leu Met Asp Arg Gly Met Glu Ile
      20              25              30
Ala Asp Phe Leu Val Pro Gln Glu Lys Thr Glu Glu Phe Phe Tyr Ala
      35              40              45
Ile Leu Gly
      50

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala
 1             5             10             15
Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala
          20             25             30
Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro
      35             40             45
Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln
      50             55             60
Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln
      65             70             75             80
Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro
          85             90             95
Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu
          100             105             110
Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp
          115             120             125
Phe Val Lys
      130

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

Met Phe Val Glu Ala Cys Lys Ala Val Val Arg Ala Asn Glu Glu Tyr
 1             5             10             15
Val Pro Pro Tyr Gly Ile Gly Gly Thr Leu Tyr Leu Arg Pro Leu Leu
          20             25             30
Ile Gly Val Gly Asp Ile Ile Gly Val Lys Pro Ala Glu Glu Tyr Ile
      35             40             45
Phe Thr Ile Phe Ala Met Pro Val Gly Asn Tyr Phe Lys Gly Gly Leu
      50             55             60

```

```

Val Pro Thr Asn Phe Leu Ile Gln Asp Glu Tyr Asp Arg Ala Ala Pro
65              70              75              80
Asn Gly Thr Gly Ala Ala Lys Val Gly Gly Asn Tyr Ala Ala Ser Leu
            85              90              95
Leu Pro Gly Lys Met Ala Lys Ser Arg His Phe Ser Asp Val Ile Tyr
            100             105             110
Leu Asp Pro Ser Thr His Thr Lys Ile Glu Glu Val Gly Ser Ala Asn
            115             120             125
Phe Phe Gly Ile Thr Ala Asp Asn Glu Phe Val Thr Pro Leu Ser Pro
            130             135             140
Ser Ile Leu Pro Ser Ile Thr Lys Tyr Ser Leu Leu Tyr Leu Ala Glu
145             150             155             160
His Arg Leu Gly Leu Thr Pro Ile Glu Gly Asp Val Pro Ile Asp Asn
            165             170             175
Leu Asp Arg Phe Val Lys Ala Gly Ala Cys Gly Thr Ala Ala Val Ile
            180             185             190
Ser Pro Ile Gly Gly Ile Gln His Gly Asp Asp Phe His Val Ile Leu
            195             200             205

```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

Met Val Met Ile Ser Met Leu Phe Tyr Ser Glu Thr Glu Val Gly Pro
1              5              10              15
Val Thr Arg Lys Leu Tyr Asn Glu Leu Thr Gly Ile Gln Phe Gly Asp
            20              25              30
Ile Glu Ala Pro Glu Gly Trp Ile Val Lys Val Asp
            35              40

```

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```

Met Thr Ala Ser Pro Leu Lys Lys Ser Ile Lys Lys Lys Asn Arg Lys
 1           5           10           15
Leu Thr Asn Lys Xaa Glu Lys His Met Ser Lys Ile Ile Gly Ile Asp
      20           25           30
Leu Gly Thr Thr Asn Ser Ala Val Ala Val Leu Glu Gly Thr Glu Ser
      35           40           45
Lys Ile Ile Ala Asn Pro Glu Gly Asn Arg Thr Thr Pro Ser Val Val
      50           55           60
Ser Phe Lys Asn Gly Glu Ile Ile Val Gly Asp Ala Ala Lys Arg Gln
      65           70           75           80
Ala Val Thr Asn Pro Asp Thr Val Ile Ser Ile Lys Ser Lys Met Gly
      85           90           95
Thr Ser Glu Lys Val Ser Ala Asn Gly Lys Glu Tyr Thr Pro Gln Glu
      100          105          110
Ile Ser Ala Met Ile Leu Gln Tyr Leu Lys Gly Tyr Ala Glu Asp Tyr
      115          120          125
Leu Gly Glu Lys Val Thr Lys Ala Val Ile Thr Val Pro Ala Tyr Phe
      130          135          140
Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Lys Ile Ala Gly
      145          150          155          160
Leu Glu Val Xaa Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala
      165          170          175
Tyr Gly Leu Asp Lys Thr Asp Lys Glu Glu Lys Ile Leu Val Phe Asp
      180          185          190
Leu Gly Gly Gly Thr Phe Asp Val Ser Ile Leu Glu Leu Gly Asp Gly
      195          200          205
Val Phe Asp Val Leu Ser Thr Ala Gly Asp Asn Lys Leu Gly Gly Asp
      210          215          220
Asp Phe Asp Gln Lys Ile Ile Asp His Leu Val Ala Glu Phe Lys Lys
      225          230          235          240
Glu Asn Gly Ile Arg Leu Val Tyr
      245

```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```

Met Lys Leu Ile Val Asp Leu Ile Tyr Glu Gly Gly Phe Lys Lys Met
 1             5             10             15
Arg Gln Ser Ile Ser Asn Thr Ala Glu Tyr Gly Asp Tyr Val Ser Gly
      20             25             30
Pro Arg Val Ile Thr Glu Gln Val Lys Glu Asn Met Lys Ala Val Leu
      35             40             45
Ala Asp Ile Gln Asn Gly Lys Phe Ala Asn Asp Phe Val Asn Asp Tyr
      50             55             60
Lys Ala Gly Arg Pro Lys Leu Thr Ala Tyr Arg Glu Gln Ala Ala Asn
65             70             75             80
Leu Glu Ile Glu Lys Val Gly Ala Glu Leu Arg Lys Ala Met Pro Phe
      85             90             95
Val Gly Lys Asn Asp Asp Ala Phe Lys Ile Tyr Asn
      100             105

```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```

Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
 1             5             10             15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
      20             25             30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
      35             40             45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
      50             55             60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
65             70             75             80

```

```

Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
      85                      90                      95
Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
      100                    105                    110
Ser Thr Ala Tyr Asn
      115

```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

Met Gly Ala Gln Leu Ala Arg Glu Phe Lys His Glu Ala Asp Ile Val
 1                      5                      10                      15
Val Gly Val Pro Asn Ser Ser Leu Ser Ala Ala Met Gly Phe Ala Glu
      20                      25                      30
Glu Ser Gly Leu Pro Asn Glu Met Gly Leu Ile Lys Asn Gln Tyr Thr
      35                      40                      45
Gln Arg Thr Phe Ile Gln Pro Thr Gln Glu Leu Arg Glu Gln Gly Val
      50                      55                      60
Arg Met Lys Leu Ser Ala Val Ser Gly Val Val Lys Gly Lys Arg Val
      65                      70                      75                      80
Val Met Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Arg Arg Ile
      85                      90                      95
Val Gln Leu Leu Lys Glu Ala Gly Ala Thr Glu Val His Val Ala Ile
      100                    105                    110
Gly Ser Pro Ala Leu Ala Tyr Pro Cys Phe Tyr Gly Ile Asp Ile Gln
      115                    120                    125
Thr Arg Gln Glu Leu Ile Ala Ala Asn His Thr Val Glu Glu Thr Arg
      130                    135                    140
Gln Ile Ile Gly Ala Asp Ser Leu Thr Tyr Leu Ser Ile Asp Ser Leu
      145                    150                    155                    160
Ile Glu Ser Ile Gly Ile Glu Thr Asp Ala Pro Asn Gly Gly Leu Cys
      165                    170                    175
Val Ala Tyr Phe Asp Gly Asp Tyr Pro Thr Pro Leu Tyr Asp Tyr Glu
      180                    185                    190

```

Glu Asp Tyr Arg Arg Ser Leu Glu Glu Lys Thr Ser Phe Tyr Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
 1 5 10 15
 Asn Pro Ala Leu Glu Ala Val Lys Leu Pro Ser Glu Ile Asn Gly
 20 25 30
 Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
 35 40 45
 Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
 50 55 60
 Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
 65 70 75 80
 Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
 85 90 95
 Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
 100 105 110
 Ser Leu Pro Ile Lys Ala Met Val Gln Ala Asn Lys Lys Glu Gly Leu
 115 120 125
 Thr Gly Ser Leu Phe Pro Ile Arg Ala Gly Thr Phe Val Cys Ser His
 130 135 140
 Leu Met Tyr Gln Ala Leu Tyr Leu Val Glu Lys Lys Phe Pro Tyr Val
 145 150 155 160
 Lys Ala Gly Phe Met His Ile Pro Tyr Met Met Glu Gln Val Val Asn
 165 170 175
 Arg Pro Thr Thr Pro Thr Met Ser Leu Val Asp Ile Arg Arg Gly Ile
 180 185 190
 Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly Asp Gln Glu Leu Thr
 195 200 205
 Leu Val Gly Gly Glu Ile His
 210 215

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```

Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly Lys
 1             5             10             15
Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu Tyr
                20             25             30
Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile Glu
                35             40             45
Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys Val
                50             55             60
Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile Gly
65             70             75             80
Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Ala Pro
                85             90             95
Val Lys Arg Gly Lys Val Met Phe Glu Ile Ala Gly Val Ser Glu Glu
                100            105            110
Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val
                115            120            125

```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```

Met Gly Trp Trp Arg Glu Thr Ile Asp Ile Val Lys Glu Asn Asp Pro
 1             5             10             15

```

```

Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr Tyr Pro Gly Val Lys
      20                      25                      30
Ala Leu Ala Ala His Arg Leu Ser His Phe Leu Trp Lys Tyr Asp Phe
      35                      40                      45
Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp Arg Phe Trp Thr Gln
      50                      55                      60
Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser Gly Val Phe Ile Asp
      65                      70                      75                      80
His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala Ile Val Glu Lys Gly
      85                      90                      95
Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Asp Cys
      100                     105                     110
Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala Leu Ile Ser Ala His
      115                     120                     125
Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu Asn Ala Lys Val Gly
      130                     135                     140
Ala Ala Ala Val Val Val Ala Asp Val Pro Ser Asp Val Thr Val Val
      145                     150                     155                     160
Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly Lys Lys Asp Glu Pro
      165                     170                     175
Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr Tyr Val Asn Lys Leu
      180                     185                     190
Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser Gly Leu
      195                     200                     205

```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Met Leu Phe Tyr Leu Leu Arg Asp Gly Lys Gly Leu Arg Asn Tyr Leu
  1                      5                      10                      15
Thr Gln Phe Ile Pro Ser Lys Leu Lys Glu Pro Val Gly Gln Val Leu
      20                      25                      30
Ser Asp Val Asn Gln Gln Leu Ser Asn Tyr Val Arg Gly Gln Val Thr
      35                      40                      45

```

```

Val Ala Ile Ile Val Ala Val Met Phe Ile Ile Phe Phe Lys Ile Ile
  50                      55                      60
Gly Leu Arg Tyr Ala Val Thr Leu Gly Val Thr Ala Gly Ile Leu Asn
  65                      70                      75                      80
Leu Val Pro Tyr Leu Gly Ser Phe Leu Ala Met Leu Pro Ala Leu Val
                      85                      90                      95
Leu Gly Leu Ile Ala Gly Pro Val Met Leu Leu Lys Val Val Ile Val
                      100                      105                      110
Phe Ile Val Glu Gln Thr Ile Glu Gly Arg Phe Val Ser Pro Leu Ile
                      115                      120                      125
Leu Gly Ser Gln Leu Asn Ile His Pro Ile Asn Val Leu Phe Val Leu
                      130                      135                      140
Leu Thr Ser Gly Ser Met Phe Gly Ile Trp Gly Val Leu Leu Gly Ile
  145                      150                      155                      160
Pro Val Tyr Ala Ser Ala Lys Val Val Ile Ser Ala Ile Phe Glu Trp
                      165                      170                      175
Tyr Lys Val Val Ser Gly Leu Tyr Glu Leu Glu Gly Glu Glu Val Lys
                      180                      185                      190
Ser Glu Gln
                      195

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Thr Lys Gln Val Pro Lys Phe Thr Lys Asp Thr Ala Gln Leu Tyr
  1                      5                      10                      15
Thr Cys Lys Trp Leu Leu Tyr Asn Lys Val Thr Lys Met Tyr Asp His
                      20                      25                      30
Thr Val Val Asn His Ser Val Arg Glu Tyr Ile Thr Asp Ser Ile Ser
                      35                      40                      45
Thr Asn Thr Ile Glu Glu Thr Gly
  50                      55

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Met Lys Lys Arg Ala Ile Val Ala Val Ile Val Leu Leu Leu Ile Gly
 1             5             10             15
Leu Asp Gln Leu Val Lys Ser Tyr Ile Val Gln Gln Ile Pro Leu Gly
          20             25             30
Glu Val Arg Ser Trp Ile Pro Asn Phe Val Ser Leu Thr Tyr Leu Gln
          35             40             45
Asn Arg Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Leu Leu Phe
 50             55             60
Ala Val Ile Thr Leu Val Val Val Ile Gly Ala Ile Trp Tyr Leu His
65             70             75             80
Lys His Met Glu Asp Ser Phe Trp Met Val Leu Gly Leu Thr Leu Ile
          85             90             95
Ile Ala Gly Gly Leu Gly Asn Phe Ile Asp Arg Val Ser Gln Gly Phe
          100             105             110
Val Val Asp Met Phe His Leu Asp Phe Ile Asn Phe Ala Ile Phe Asn
          115             120             125
Val Ala Asp Asn Tyr Leu Thr Val Gly Val Ile Ile Leu Leu Ile Ala
          130             135             140
Met Leu Lys Glu Glu Ile Asn Gly Asn
145             150

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
 1             5             10             15
Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
             20             25             30
Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
             35             40             45
Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
             50             55             60
Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
65             70             75             80
Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Thr Tyr Val
             85             90             95
Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
             100             105

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys Phe Ala
 1             5             10             15
Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val Ala Gly
             20             25             30
Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val Ser Val
             35             40             45
Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe Gly Gly
             50             55             60
His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val Gly Ala
65             70             75             80
Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln Tyr Leu
             85             90             95
Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu Lys Ala
             100             105             110
Glu

```


(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala His Val Ala Cys
 1             5             10             15
Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His Ala Glu Ser Leu
          20             25             30
Gly Val Asp Ala Ile Ala Thr Asp Ser Thr Asn Leu Phe Pro Leu Ala
          35             40             45
Arg Ile Thr Gln Leu Pro Asn Thr Gly Thr Ile Ser Val Leu Gln Leu
          50             55             60
Gln Thr Gln Thr Thr
65

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Met Gly Glu Thr Gln Ile Ile Asp Gly Leu Asp Pro Glu Tyr Lys Lys
 1             5             10             15
Arg Phe Met His His Tyr Asn Phe Pro Gln Tyr Ser Val Gly Glu Thr
          20             25             30
Gly Arg Tyr Gly Ala Pro Gly Arg Arg Glu Ile Gly His Gly Ala Leu
          35             40             45
Gly Glu Arg Ala Leu Ala Gln Val Leu Pro Ser Leu Glu Glu Phe Pro
          50             55             60

```

```

Tyr Ala Ile Arg Leu Val Ala Glu Val Leu Glu Ser Asn Gly Ser Ser
65          70          75          80
Ser Gln Ala Ser Ile Cys Ala Gly Thr Leu Ala Leu Met Ala Gly Gly
          85          90          95
Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu Ile Ser
          100          105          110
Asp Gly Asn Asn Tyr Thr Val Leu Thr Asp Ile Gln Gly Leu Glu Asp
          115          120          125
His Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Arg Asp Gly Ile
          130          135          140
Thr Ala Leu Gln Met Asp Ile Lys Ile Gln Gly Ile Thr Ala Glu Ile
145          150          155          160
Leu Thr Glu Ala Leu Ala Gln Ala Lys Lys Ala Arg Phe Glu Ile Leu
          165          170          175
Asp Val Ile Glu Ala Thr Ile Pro Glu Val Arg Pro Glu Leu Ala Pro
          180          185          190
Thr Ala Pro Lys Ile Asp Thr Ile Lys Ile Asp Val Asp Lys Ile Lys
          195          200          205
Ile Val Ile Gly Lys Gly Gly Glu Thr Ile Asp Lys Ile Ile Ala Glu
          210          215          220
Thr Gly Val Lys Ile Asp Ile Asp Glu Glu Xaa Asn Val Phe Tyr Leu
225          230          235          240
Leu Leu Val Asp Gln Asn Ala Ile Asn Pro Cys Pro Lys Lys Leu Leu
          245          250          255
Leu Val Trp Phe Arg Glu Pro Lys Trp Met Lys Phe Thr Val Leu Asn
          260          265          270
Arg Ser Tyr Arg Glu Phe Gly Ala Phe Val Thr Leu
          275          280

```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

Met Ile Asn Asn Val Val Leu Val Gly Arg Met Thr Arg Asp Ala Glu
1          5          10          15

```

```

Leu Arg Tyr Thr Pro Ser Asn Val Ala Val Ala Thr Phe Thr Leu Ala
      20                      25                      30
Val Asn Arg Thr Phe Lys Ser Gln Asn Gly Glu Arg Glu Ala Asp Phe
      35                      40                      45
Ile Asn Val Val Met Trp Arg Gln Gln Ala Glu Asn Leu Ala Asn Trp
      50                      55                      60
Ala Lys Lys Gly Ser Leu Ile Gly Val Thr Gly Arg Ile Gln Thr Arg
      65                      70                      75                      80
Ser Tyr Asp Asn Gln Gln Gly Gln Arg Val Tyr Val Thr Glu Val Val
      85                      90                      95
Ala Glu Asn Phe Gln Met Leu Glu Ser Arg Ser Val Arg Glu Gly His
      100                     105                     110
Thr Gly Gly Ala Tyr Ser Ala Pro Thr Ala Asn Tyr Ser Ala Pro Thr
      115                     120                     125
Asn Ser Val Pro Asp Phe Ser Arg Asn Glu Asn Pro Phe Gly Ala Thr
      130                     135                     140
Asn Pro Leu Asp Ile Ser Xaa Asp Asp Leu Pro Phe
      145                     150                     155

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Met Asp Leu Val Arg Ile Leu Lys Glu Pro Arg Asn Ala Leu Val Lys
1           5           10           15
Gln Tyr Gln Thr Leu Leu Ser Tyr Asp Asp Val Glu Leu Glu Phe Asp
      20           25           30
Asp Glu Ala Leu Gln Glu Ile Ala Asn Lys Ala Ile Glu Arg Lys Thr
      35           40           45
Gly Ala Arg Gly Leu Arg Ser Ile Ile Glu Glu Thr Met Leu Asp Val
      50           55           60
Met Phe Glu Val Pro Ser Gln Glu Asn Val Lys Leu Val Arg Ile Thr
      65           70           75           80
Lys Glu Thr Val Asp Gly Thr Asp Lys Pro Ile Leu Glu Thr Ala
      85           90           95

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Met Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu Leu
 1             5             10             15
Lys Leu Leu Gln Val Ala Asp Phe Asn Ile Glu Arg Ala Glu Arg Gly
      20             25             30
Ile Ile Tyr Val Asp Glu Ile Asp Lys Ile Ala Lys Lys Ser Glu Asn
      35             40             45
Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala Leu
      50             55             60
Leu Lys Ile Ile Glu Gly Thr Val Ala Ser Val Pro Pro Gln Gly Gly
      65             70             75             80
Arg Lys His Pro Gln Val Asp Asp Ser Ser Gly Tyr Lys Lys Tyr
      85             90             95
Pro Leu His Arg Gly Trp Cys Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Met Trp Pro Arg Glu Ser Arg Ser Cys Arg Leu Thr Lys Val Lys Ile
 1             5             10             15

```

Cys Gly Leu Ser Thr Lys Glu Ala Val Glu Thr Ala Val Ser Ala Gly
 20 25 30
 Ala Asp Tyr Ile Gly Phe Val Phe Ala Pro Ser Lys Arg Gln Val Thr
 35 40 45
 Leu Glu Glu Ala Ala Glu Leu Ala Lys Leu Ile Pro Ala Asp Val Lys
 50 55 60
 Lys Val Gly Val Phe Val Ser Pro Ser Arg Val Glu Leu Leu Glu Ala
 65 70 75 80
 Ile Asp Lys Val Gly Leu Asp Leu Val Gln Val His Gly Gln Val Ala
 85 90 95
 Asp Asp Leu Phe Glu Asn Leu Pro Cys Ala Ser Ile Gln Ala Val Gln
 100 105 110
 Val Asp Gly Asn Gly His Val Pro Asn Ser Gln Ala Asp Tyr Leu Leu
 115 120 125
 Phe Asp Ala Pro Val Ala Gly Ser Gly Gln Ser Phe Asp Trp Gly Gln
 130 135 140
 Leu Asp Thr Thr Gly Leu Ala Gln Pro Phe Phe Ile Ala Gly Gly Leu
 145 150 155 160
 Asn Glu Asp Asn Val Val Lys Ala Ile Gln His Phe Thr Pro Tyr Ala
 165 170 175
 Val Asp Val Ser Ser Gly Val Glu Thr Asp Gly Gln Lys Asp His Glu
 180 185 190
 Lys Ile Arg Arg Phe Ile Glu Arg Val Lys His Gly Ile Ser Gly Thr
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30

```

Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
   35               40               45
Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
   50               55               60
Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
   65               70               75               80
Tyr Xaa Phe Met Arg Asp Ala Ala Ala Asn Asp Ala Val Val Leu Phe
               85               90               95
Val Gly Thr Lys Lys Thr Ser Ser
               100

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp Val Ile Ile Pro
   1               5               10               15
Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile Thr Ala Lys Leu
               20               25               30
Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp Ala Val Ala Val
               35               40               45

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Met Glu Glu Leu Gly Gln Ser Tyr Gly Tyr Leu Leu Tyr Arg Thr Glu
   1               5               10               15

```

Thr Asn Trp Asp Ala Glu Glu Arg Leu Arg Ile Ile Asp Gly Arg
 20 25 30
 Asp Arg Ala Gln Leu Tyr Val Asp Gly Gln Trp Val Lys Thr Gln Tyr
 35 40 45
 Gln Thr Glu Ile Gly Glu Asp Ile Phe Tyr Gln Gly Lys Lys Lys Gly
 50 55 60
 Leu Ser Arg Leu Asp Ile Leu Ile Glu Asn Met Gly Arg Val Asn Tyr
 65 70 75 80
 Gly His Lys Phe Leu Ala Asp Thr Gln Arg Lys Gly Ile Arg Thr Gly
 85 90 95
 Val Cys Lys Asp Leu His Phe Leu Leu Asn Trp Lys His Tyr Pro Leu
 100 105 110
 Pro Leu Asp Asn Pro Glu Lys Ile Asp Phe Ser Lys Gly Trp Thr Gln
 115 120 125
 Gly Gln Pro Ala Phe Tyr Ala Tyr Asp Phe Thr Val Glu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
 1 5 10 15
 Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
 20 25 30
 Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
 35 40 45
 Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
 50 55 60
 Arg Leu Ala Arg
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val Ala Ala
 1             5             10             15
Val Gly Leu Ala Ala Cys Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser
          20             25             30
Ser Ser Asp Val Lys Thr Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
          35             40             45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Val Ala Gly Leu
 50             55             60
Gly
65

```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Met Ser Gln Trp Asp Arg Lys Leu Asp Ala Arg Leu Ala Gln Ala Val
 1             5             10             15
Val Ser Ile Asn Ala Phe Lys Gly Val Glu Phe Gly Leu Gly Phe Glu
          20             25             30
Ala Gly Tyr Arg Lys Gly Ser Gln Val Met Asp Glu Ile Leu Trp Ser
          35             40             45
Lys Glu Asp Gly Tyr Thr Arg Arg Thr Asn Asn Leu Gly Gly Phe Glu
 50             55             60
Gly Gly Met Thr Asn Gly Gln Pro Ile Val Val Arg Gly Val Met Lys
 65             70             75             80
Pro Ile Pro Thr Leu Tyr Lys Pro Leu Met Ser Val Asp Ile Glu Thr
          85             90             95

```


His Glu Pro Tyr Lys Ala Thr Val Glu Arg Ser Asp Pro Thr Ala Leu
 100 105 110
 Pro Ala Ala Gly Met Val Met Glu Ala Val Val Ala Thr Val Leu Ala
 115 120 125
 Gln Glu Ile Leu Glu Lys Phe Ser Ser Asp Asn Leu Glu Glu Leu Lys
 130 135 140
 Glu Ala Val Ala Lys His Arg Asp Tyr Thr Lys Asn Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
 1 5 10 15
 Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
 20 25 30
 Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
 35 40 45
 Asn Lys Lys Tyr Thr Val Leu Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
 1 5 10 15

Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
 20 25 30
 Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
 35 40 45
 Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Phe Thr Lys Lys Leu
 50 55 60
 Glu
 65

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Met Glu Ser Gly Ala Thr Ala Val Val Ala Glu Arg Gly Gln
 1 5 10 15
 Glu Arg Ile Thr Lys Val Arg Glu Ile Leu Gly Gly Gly Ala Asp Ala
 20 25 30
 Ala Leu Glu Cys Val Gly Thr Glu Ala Ala Ile Glu Gln Ala Leu Gly
 35 40 45
 Val Leu His Asn Gly Gly Arg Met Gly Phe Val Gly Val Pro His Tyr
 50 55 60
 Asn Asn Arg Ala Leu Gly Ser Thr Phe Met Gln Asn Ile Ser Val Ala
 65 70 75 80
 Gly Gly Ala Ala Ser Ala Thr Thr Tyr Asp Lys Gln Phe Leu Leu Lys
 85 90 95
 Ala Val Leu Asp Gly Asp Ile Asn Pro Gly Arg Val Phe Thr Ser Ser
 100 105 110
 Tyr Lys Leu Glu Asp Ile Asp Gln Ala Tyr Lys Asp Met Asp Glu Arg
 115 120 125
 Lys Thr Ile Lys Ser Met Ile Val Ile Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Met Lys Gln Val Val Asp Tyr Phe Leu Ser Gln Gly Met Asp Arg Ile
 1             5             10             15
Gly Ile Leu Thr Gly Leu Glu Glu Thr Thr Asp Gln Glu Glu Ile Ile
      20             25             30
Gln Asp Lys Arg Leu Glu Asn Phe Lys Asn Tyr Ser Gln Ala Arg Gly
      35             40             45
Ile Tyr His Asp Glu Leu Val Phe Gln Gly Arg Phe Thr Ala Gln Ser
      50             55             60
Gly Tyr Asp Leu Met Lys Glu Ala Ile Gln Ser Leu Gly Asp Gln Leu
      65             70             75             80
Pro Pro Ala Phe Phe Ala Ala Ser Asp Ser Leu Ala Ile Gly Ala Leu
      85             90             95
Arg Ala Leu Gln Glu Ala Gly Ile Ser Leu Pro Asp Arg Val Ser Leu
      100            105            110
Ile Phe Leu Leu Thr Thr Leu Ser Leu Thr Lys Gln Val Tyr Pro Pro
      115            120            125
Leu Ser
      130
  
```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
 1             5             10             15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
      20             25             30
  
```

```

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Glu Ile Val
   35                40                45
Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr
   50                55                60
Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val
   65                70                75                80
Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val
                85                90                95
Leu Asp Leu Ala Glu Ser Leu Leu Asp
                100                105

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala
  1                5                10                15
Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val
                20                25                30
Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp
                35                40                45
Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser
                50                55                60
Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn
   65                70                75                80
Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly
                85                90                95
Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg
                100                105                110
Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg
                115                120                125

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Met Ser Ala Ile Asn Leu Ala Ser Val Pro Lys Glu Ser Leu Thr Gln
 1             5             10             15
Val Leu Pro Arg Asp Leu His Ala Glu Tyr Phe Ala Val Leu Ala Ser
      20             25             30
Ile Ala Thr Ser Ile Glu Arg Met Ala Thr Glu Ile Arg Gly Leu Gln
      35             40             45
Lys Ser Glu Gln Arg Glu Val Glu Glu Phe Phe Ala Lys Gly Gln Lys
      50             55             60
Gly Ser Ser Ala Met Pro His Lys Arg Asn Pro Ile Gly Ser Glu Asn
      65             70             75             80
Met Thr Gly Leu Ala Arg Val Ile Arg Gly His Met Ile Thr Ala Tyr
      85             90             95
Glu Asn Val Ala Leu Trp His Glu Arg Asp Ile Ser His Ser Ser Ala
      100            105            110
Glu Arg Ile Ile Thr Pro Asp Thr Thr Ile Leu Ile Asp Tyr Met Leu
      115            120            125
Asn Arg Phe Gly Asn Ile Val Lys Asn Leu Thr Val Phe Pro Glu Asn
      130            135            140
Met Ile Arg Asn Met Asn Ser Thr Phe Gly Leu Ile Phe Ser Gln Arg
      145            150            155            160
Ala Met Leu Thr Leu Ile Glu Lys Gly Met Thr Arg Glu Gln Ala Tyr
      165            170            175
Asp Leu Val Gln Pro Lys Thr Ala Tyr Ser Trp Asp Asn Gln Val Asp
      180            185            190
Phe Lys Pro Leu Leu Glu Ala Asp Ser Glu Val Thr Ser Arg Leu Thr
      195            200            205
Gln Glu Glu Ile Asp Glu Ile Phe Asn Pro Val Tyr Tyr Thr Lys Arg
      210            215            220
Val Asp Asp Ile Phe Glu Arg Leu Gly Leu Gly Asp
      225            230            235

```

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Met Leu Asn Leu Thr His Val Thr Leu Lys Thr Arg Gln Val Ile Leu
 1             5             10             15
Gln Asp Ala Asp Phe Thr Phe Lys Lys Gly Arg Ile Tyr Gly Leu Leu
      20             25             30
Ala Ile Asn Gly Ser Gly Lys Thr Thr Leu Phe Arg Ala Met Ser Lys
      35             40             45
Leu Leu Pro Leu Ser Ser Gly His Ile Ala Val Pro Pro Ser Leu Phe
      50             55             60
Tyr Tyr Glu Ser Val Glu Trp Leu Asp Gly Asn Leu Ser Gly Met Asp
65             70             75             80
Tyr Leu Arg Leu Ile Lys Lys His Leu Glu Val Arg Pro Lys Leu Glu
      85             90             95
Arg

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala Glu Phe Leu Asn
 1             5             10             15
Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val Lys Gly Leu Lys
      20             25             30
Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp Ala Ala Gly Thr
      35             40             45
Val Thr Val Leu Glu Gly Arg Gln
      50             55

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Met Asn Gln Glu Glu Leu Ala Lys Lys Met Leu Leu Pro Ser Lys Asn
 1             5             10             15
Ser Arg Leu Glu Lys Leu Gly Lys Gly Leu Thr Phe Ala Cys Leu Ser
          20             25             30
Leu Ile Val Ile Leu Val Ala Met Ile Leu Val Phe Val Ala Gln Lys
          35             40             45
Gly Leu Ser Thr Phe Phe Val Asn Gly Val Asn Ile Phe Asp Phe Leu
          50             55             60
Leu Gly Gly Thr Trp Asn Pro Ser Ser Lys Glu Phe Gly Ala Leu Pro
65             70             75             80
Met Ile Leu Gly Ser Phe Ile Val Thr Ile Leu Ser Ala Leu Ile Ala
          85             90             95
Thr Pro Phe Ala Ile Gly Ala Ala Val Phe Met Thr Glu Val Ser Pro
          100            105            110
Lys Gly Ala Lys Ile Leu Gln Pro Ala Ile Glu Leu Leu Val Gly Ile
          115            120            125
Pro Ser Val Val Tyr Gly Phe Ile Gly Leu Gln Val Val Val Pro Phe
          130            135            140
Val Arg Ser Val Phe Gly Gly Thr Gly Phe Gly Ile Leu Ser Gly Ile
145            150            155            160
Ser Val Leu Phe Val Met Ile Leu Pro Thr Val Thr Phe Met Thr Thr
          165            170            175
Asp Ser Leu Arg Ala Val Pro Xaa Leu Leu Ser
          180            185

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
 1           5           10           15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
      20           25           30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
      35           40           45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
      50           55           60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
      65           70           75           80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
      85           90           95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
      100          105          110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
      115          120          125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
      130          135          140
Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp
      145          150          155          160
Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys
      165          170          175
Gln Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala
      180          185          190
Leu Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln
      195          200          205
Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu
      210          215          220
Val Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu
      225          230          235          240
Asp Lys

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

Met Glu His Pro Xaa Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro
 1           5           10           15
Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu
          20           25           30
Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala
          35           40           45
Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu
          50           55           60
Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys
65           70           75

```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Val Tyr Thr Ser Leu Ser Ser Lys Asp Gly Asn Tyr Pro Tyr Gln
 1           5           10           15
Leu Asn Ile Ala His Leu Tyr Gly Asn Leu Met Asn Thr Tyr Gly Asp
          20           25           30
Asn Gly Asn Ile Leu Met Leu Lys Tyr Val Ala Glu Lys Leu Gly Thr
          35           40           45
His Val Thr Val Asp Ile Val Ser Leu His Asp Asp Phe Asp Glu Asn
          50           55           60
His Tyr Asp Ile Ala Phe Phe Gly Gly Gly Gln Asp Phe Glu Gln Ser
65           70           75           80
Ile Ile Ala Asp Asp Leu Pro Ala Lys Lys Glu Ser Ile Asp Asn Tyr
          85           90           95
Ile Gln Asn Asp Gly Val Val Leu Ala Ile Cys Gly Gly Phe Gln Leu
          100          105          110
Leu Gly Gln Tyr Tyr Val Glu Ala Ser Gly Lys Arg Ile Glu Gly Leu
          115          120          125

```

Gly Val Met Gly His Tyr Thr Leu Asn Gln Thr Asn Asn Arg Phe Ile
 130 135 140
 Gly Asp Ile Lys Ile His Asn Glu Arg Phe Arg
 145 150 155

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met His Gln His Ser Pro His Thr Ala Ser Tyr Thr Ser Ser Arg Asp
 1 5 10 15
 Ala Met Ser Lys Tyr Pro Glu Arg Cys Thr Thr Val Gly Leu Arg Leu
 20 25 30
 Asn Glu Glu Ser Asp Phe Glu Leu Tyr Ala Pro Tyr Gly Leu Glu Asp
 35 40 45
 Ile Leu Asn Phe Lys Phe Val Gln Leu Leu Ile Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Phe Glu Ile Phe Asn Met Gly Val Gly Leu Met Leu Ala Val Ser
 1 5 10 15
 Pro Glu Asn Val Glu Arg Val Lys Glu Leu Leu Asp Glu Ala Val Tyr
 20 25 30
 Glu Ile Gly Arg Ile Val Lys Lys Glu Asn Glu Ser Val Ile Ile Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Met Met Val Lys Lys His Tyr Phe Lys Asp Asn Glu Glu Asp Ser Lys
 1             5             10             15
Met Arg Arg Ile Leu Leu Leu Val Ala Val Leu Leu Met Ile Pro Ser
          20             25             30
Phe Ile Ser Ala Thr Thr Leu Val Arg Glu Thr Leu Lys Lys Glu Ser
          35             40             45
Leu Lys Lys Phe Ile Ser Glu Gln Phe Gln Gly His Asn Ile Leu Lys
 50             55             60
Lys Thr Tyr Ser Lys Lys Thr His Thr Leu Lys Leu Thr Ile Ser Gly
65             70             75             80
Asn Tyr Leu Thr Glu Glu Glu Leu Asp Met Ile Ser Ser Lys Arg Gly
          85             90             95
Asp Tyr Gly Leu Ser Asp Val Ser Val Gln Val Ser Gln Leu Ser Asp
          100            105            110
Ser Glu Gln Leu Ser Lys Glu Glu Leu Val Glu Tyr Phe Phe Gln Tyr
          115            120            125
Ile Lys Asp Lys Glu Ala Lys Glu Lys Glu Lys Ala Asn Lys Phe Tyr
          130            135            140
Thr Glu Ser Glu Glu Gln
145            150

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

Met Ser Ile Glu Pro Arg Arg Arg Trp Arg Asn Ser Thr Val Cys Leu
 1           5           10           15
Glu Ala Glu Leu Tyr Gln Glu Ser Leu Val Leu Ile Gly Gly Asp Pro
          20           25           30
Gly Ile Gly Lys Ser Thr Leu Leu Leu Gln Val Ser Thr Gln Leu Ser
          35           40           45
Gln Val Gly Thr Val Leu Tyr Val Ser Gly Glu Glu Ser Ala Gln Gln
          50           55           60
Ile Lys Leu Arg Ala Glu Arg Leu Gly Asp Phe Asp Ser Glu Phe Tyr
65           70           75           80
Leu Tyr Ala Glu Thr Asn Met Gln Ser Val Arg Ala Glu Val Val Ala
          85           90           95
Tyr Pro Ala Arg Leu Ser His Tyr
          100

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

Met Ala Thr Lys Gln Lys Glu Val Thr Thr Phe Asp Val Gln Val Ala
 1           5           10           15
Glu Phe Ile Arg Asn His Lys Gln Lys Gly Thr Ala Thr Asp Asp Glu
          20           25           30
Ile Asn Ala Ser Leu Val Ile Pro Phe Thr Leu Asp Ala Asp Gly Ile
          35           40           45
Glu Asp Leu Leu Gln Arg Ile Gln Asp Ala Gly Ile Ser Ile Thr Asp
          50           55           60
Asn Glu Gly Asn Pro Ser Ala Arg Val Leu Ser Asn Glu Glu Glu Pro
65           70           75           80
Glu Leu Ser Asp Glu Asp Leu Ile Gly Ser Thr Ser Ala Lys Val Asn
          85           90           95
Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Val Val Pro Leu Leu
          100           105           110

```

Thr Asn Glu Glu Glu Lys Glu Leu Ala Leu Ala Val Glu Ala Gly Asp
 115 120 125
 Ile Glu Ala Lys Gln Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140
 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Xaa Gln Ser Leu Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Met Leu Lys Pro Ser Ile Asp Thr Leu Leu Asp Lys Val Pro Ser
 1 5 10 15
 Lys Tyr Ser Leu Val Ile Leu Glu Ala Lys Arg Ala His Glu Leu Glu
 20 25 30
 Ala Gly Ala Pro Ala Thr Gln Gly Phe Lys Ser Glu Lys Ser Thr Leu
 35 40 45
 Arg Ala Leu Glu Glu Ile Glu Ser Gly Asn Val Thr Ile His Pro Asp
 50 55 60
 Pro Glu Gly Lys Arg Glu Ala Val Arg Arg Arg Ile Glu Glu Glu Lys
 65 70 75 80
 Arg Arg Lys Glu Glu Glu Glu Lys Lys Ile Lys Glu Gln Ile Ala Lys
 85 90 95
 Glu Lys Glu Asp Gly Glu Lys Ile
 100

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Ile Arg Gln Gly Gln Met Leu Glu Tyr Ala Glu Tyr Val Gly Asn
 1           5           10           15
Tyr Tyr Gly Thr Pro Leu Thr Tyr Val Asn Glu Thr Leu Asp Lys Gly
          20           25           30
Ile Asp Val Phe Leu Glu Ile Glu Val Gln Gly Ala Leu Gln Val Lys
          35           40           45
Lys Lys Val Pro Asp Ala Val Phe Ile Phe Leu Thr Pro Pro Asp Leu
          50           55           60
Asp Glu Leu Gln Glu Arg Leu Val Gly Arg Gly Thr Asp Ser Ala Glu
65           70           75           80
Val Ile Ala Gln Arg Ile Glu Lys Ala Lys Glu Glu Ile Ala Leu Met
          85           90           95
Arg Glu Tyr Asp Tyr Ala Ile Val Asn Asp Gln Val Pro Leu Ala Ala
          100          105          110
Glu Arg Val Lys Cys Val Ile Glu Ala Glu His Phe Cys Val Asp Arg
          115          120          125
Val Ile Gly His Tyr Gln Glu Met Leu Pro Lys Ser Pro Thr Thr Arg
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

Met Ser Arg Leu Leu Val Ile Gly Cys Gly Gly Val Ala Gln Val Ala
 1           5           10           15
Ile Ser Lys Ile Cys Gln Asp Ser Glu Thr Phe Thr Glu Ile Met Ile
          20           25           30
Ala Ser Arg Thr Lys Ser Lys Cys Asp Asp Leu Lys Ala Lys Leu Glu
          35           40           45
Gly Lys Thr Ser Thr Lys Ile Glu Thr Ala Ala Leu Asp Ala Asp Lys
          50           55           60
Val Glu Glu Val Ile Ala Leu Ile Glu Ser Leu Gln Thr Ser Lys Leu
65           70           75           80
Phe

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

Met His Glu Ser Phe His Val Asp Asp Pro Thr Leu Tyr Ser Arg Glu
 1             5             10             15
Trp Phe Ser Trp Ala Asn Met Met Phe Cys Glu Leu Val Leu Asp Tyr
          20             25             30
Leu Asp Ile Arg
          35

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

```

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
 1             5             10             15
Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
          20             25             30
Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
          35             40             45
Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
          50             55             60
Asp
65

```

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

```

Met Leu Leu Tyr Ile Leu Ser His Ile Ala Thr Gly Ile Val Ser Gly
 1           5           10           15
Thr Cys Leu Leu Lys Ala Ile Val Cys Asn Trp Trp Asn Cys Leu Thr
          20           25           30
Ile Ser Leu Ile Ser Leu Lys Met Thr Leu Ser Ser Arg Val Ser Thr
          35           40           45
Trp Met Asp Lys Leu Leu Ser Leu Thr Thr Asn Leu Gln Ile Arg Pro
          50           55           60
Glu Asn Arg Asp Lys Val Gln Arg Tyr Ile Asp Glu Gly Lys Leu Lys
65           70           75           80
Ile Gly Pro Phe Tyr Ile Leu Gln Asp Asp Tyr Leu Ile Ser Ser Glu
          85           90           95
Ala Asn Val Arg Asn Thr Leu Ile Gly Gln Gln Glu Ala Ala Lys Trp
          100          105          110
Gly Lys Ser Thr Gln Ile Gly Tyr Phe Pro Asp Thr Phe Gly Asn Met
          115          120          125
Gly Gln Ala Pro Gln Ile Leu Gln Lys Ser Gly Ile His Val Ala Ala
          130          135          140
Phe Gly Arg Gly Val Lys Pro Ile Gly Phe Asp Asn Gln Val Leu Glu
145          150          155          160
Asp Glu Gln Phe Thr Ser Gln Phe Ser Glu Met Tyr Trp Gln Gly Val
          165          170          175
Asp Gly Ser Arg Val Leu Gly Ile Leu Phe Ala Asn Trp Tyr Ser Asn
          180          185          190
Gly Asn Glu Ile Pro Val Asp Lys Asp Glu Ala Leu Thr Phe Trp Lys
          195          200          205
Gln Lys Leu Ser Asp Val Arg Cys Leu Arg Phe Asp Gln Pro Met Val
          210          215          220
Asp Asp Glu Thr Ala Val Asn Thr Ser Leu Ser Gln Lys Lys Ser Glu
225          230          235          240
Arg Ser His Ser Val Trp Gln Met Asn Ser Ser Arg Met
          245          250

```


(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```

Met Thr Ile Val Gly Cys Arg Ile Asp Gly Arg Leu Ile His Gly Gln
 1             5             10             15
Val Ala Asn Leu Trp Ala Gly Lys Leu Asn Val Ser Arg Ile Met Val
      20             25             30
Val Asp Asp Glu Val Val Asn Asn Asp Ile Glu Lys Ser Gly Leu Lys
      35             40             45
Leu Ala Thr Pro Pro Gly Val Lys Leu Ser Ile Leu Pro Val Glu Lys
      50             55             60
Ala Ala Ala Asn Ile Leu Ala Gly Lys Tyr Asp Ser Gln Arg Leu Phe
65             70             75             80
Ile Val Ala Arg Lys Pro Asp Arg Phe Pro Trp Phe Gly Arg Ser Arg
      85             90             95
Cys Thr Thr

```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Met Ile Gln His Pro Arg Ile Gly Ile Arg Pro Thr Ile Asp Gly Arg
 1             5             10             15
Arg Gln Gly Val Arg Glu Ser Leu Glu Val Gln Thr Met Asn Met Ala
      20             25             30

```

```

Lys Ser Val Ala Asp Leu Ile Ser Ser Thr Leu Lys Tyr Pro Asp Gly
      35                      40                      45
Glu Pro Val Glu Cys Val Ile Ser Pro Ser Thr Ile Gly Arg Val Pro
      50                      55                      60
Glu Ala Ala Ala Ser His Glu Leu Phe Lys Lys Ser Asn Val Cys Ala
      65                      70                      75                      80
Thr Ile Thr Val Thr Pro Cys Trp Cys Tyr Gly Ser Glu Thr Met Asp
                      85                      90                      95
Met Ser Pro Asp Ile Pro His Ala Ile Trp Gly Phe Asn Gly Thr Glu
                      100                     105                     110
Arg Pro Gly Ala Val Tyr Leu Ala Ala Val Leu Ala Ser His Ala Gln
                      115                     120                     125
Lys Gly Ile Pro Ala Phe Gly Ile Tyr Gly Arg Asp Val Gln Glu Ala
                      130                     135                     140
Asn Asp Thr Asp Ile Pro Glu Asp Val Lys Glu Asn Phe
      145                     150                     155

```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Met Leu Leu Ser Thr Lys Gly Ile Glu Glu Gln Glu Ile Ala Arg Pro
  1                      5                      10                      15
Thr Leu Glu Arg Leu Phe Ser Met Arg Glu Asn Tyr Lys Val Thr Gly
                      20                      25                      30
Arg His Pro Gly Tyr Arg Lys Tyr Asn Gly Asp Gly Ser Met Lys Glu
                      35                      40                      45
Thr Glu Lys
      50

```

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Met Leu Thr Leu Thr Pro Asp Val Ile Tyr Gln Glu Pro Asp Ile Leu
 1             5             10             15
Tyr Gln His Glu Asp Phe Ser Leu Val Lys Ile Arg Gln Ile Arg Phe
          20             25             30
Cys

```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Met Ser Ser Val Val Gly Leu Met Gly Asn Ile Gly Gln Ala Asn Tyr
 1             5             10             15
Ala Ala Ser Lys Ala Gly Leu Ile Gly Phe Thr Lys Ser Val Ala Arg
          20             25             30
Glu Val Ala Ser Arg Asn Ile Arg Val Asn Val Ile Ala Pro Gly Asn
          35             40             45
Asp

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
 1             5             10             15
Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
      20             25             30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
      35             40             45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
      50             55             60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
      65             70             75             80
Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
      85             90             95
Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
      100            105            110
Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Phe Gly Asn Arg
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

Met Glu Ser Met Pro Arg Ile Gly Leu Leu Val Thr Val Glu Asn Arg
 1             5             10             15
Asp Thr Glu Thr Ile Phe Asn Ala Ala Gly Leu Asp Phe Asp Val Leu
      20             25             30
Lys Ala Ser Ala Ile Ala Tyr Ile Asn Ala Asn Thr Phe Val Gln Lys
      35             40             45
Glu Asn Ala Gly Glu Met Gly Arg Ser Val Ser Tyr His Asp Met Arg
      50             55             60
Ser Val
      65

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Met Arg Gln Gly Gln Gly Ser Val Glu Ala Ile Phe Asn Ala Ile Asp
 1             5             10             15
Lys Phe Phe Asn Gln Ser Val Arg Leu Val Ser Tyr Thr Ile Asn Ala
      20             25             30
Val Thr Asp Gly Ile Asp Ala Gln Asp Arg Val Val Gly His Cys
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Val Glu Asn Pro Glu Gly Phe His Phe Asp Asp Leu Gln Leu Gln
 1             5             10             15
Thr His Ala Asp Asn Asp Ile Glu Ala Leu Val Ser Leu Ala Asn Met
      20             25             30
Asp Gly Glu Lys Val Glu Phe Asn Ala Thr Gly Thr Gly Phe Arg
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Asn Phe Gln Leu Ala Lys Tyr Ser Leu Leu Lys Lys Phe Ser Glu
 1             5             10             15
Asn Ile Gly Phe Thr Thr Pro Glu Glu Cys Gly Ala Ile Phe Gln Tyr
      20             25             30
Leu Ile Glu Asn Val Gln Thr Asp Arg Gln Ile Ile Tyr Ser Pro Pro
      35             40             45
Cys His Asp Glu Leu Arg Met Ala Val Ala Asn Ser Leu Ala Ala Val
      50             55             60
Lys Asn Gly Ala Gly Leu Phe Glu Glu Thr Ile His Gly Ile Arg Glu
      65             70             75             80
Arg Ala Glu Asn Ala Ala Leu Glu Glu Ile Ala Val Ala Leu Asn Ile
      85             90             95
Arg Gln Asp Tyr Tyr Gln Val Glu Thr Ser Ile Val Leu Asn Glu Thr
      100            105            110
Ile Asn Thr Ser Glu Met Val Ser Arg Phe Ser Gly Ile Pro Val Pro
      115            120            125
Lys Asn Lys Ala Val Val Gly Gly Asn Thr Phe Ser His Glu Ser Gly
      130            135            140
Ile His Gln Asp Gly Val Leu Lys Asn Pro Leu Thr Tyr Glu Ile Ile
      145            150            155            160
Thr Pro Glu Leu Val Gly Val Lys Ile Pro Leu Gly Lys Leu Ser Gly
      165            170            175
Arg His Ala Phe Val Glu Lys Leu Arg Glu Leu Ala Leu Asp Phe Thr
      180            185            190
Glu Glu Asp Ile Lys Pro Phe Phe Ala Lys Phe Lys Ala Leu Ala Asp
      195            200            205
Lys Lys
      210

```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Ser Gln Gln Val Lys Asn Ala His Asn Leu Tyr Ile His Ala Ile
 1             5             10             15
Gln Asp Gly Arg Val Ala Glu Ala Gln Ala Gln Ser Val Gly Asp Thr
      20             25             30
Tyr Ile Gln His Ser Thr Gly Val Pro Asp Gly Lys Glu Gly Phe Ala
      35             40             45
Ala Phe Phe Ala Asp Phe Phe Glu Arg His Pro Glu Arg Gln Ile Lys
      50             55             60
Ile Val Arg Thr Ile Glu Asp Gly Asn Leu Val Phe Val His Val Pro
65             70             75             80
Ser Ile Ser Glu Trp Trp Arg Ser Ser Met Gly Asp Asp Gly Tyr Phe
      85             90             95
Pro Cys Gly

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
 1             5             10             15
Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
      20             25             30
Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
      35             40             45
Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
      50             55             60
Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
65             70             75             80
Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
      85             90             95
Thr Ala Met Ile Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val
      100             105             110
Thr Phe Leu Leu Glu Gln Leu Phe Ser Ile
      115             120

```

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Met Ala Phe Phe Leu Cys Pro His Phe Arg Ser Asn His Trp Lys Ile
 1           5           10           15
Leu Thr Val Ser Asp Thr Met Glu Glu Lys Arg Leu Glu Tyr Pro Met
          20           25           30
Val Thr Phe Leu Gly Asn Pro Val Ser Phe Thr Gly Lys Gln Leu Gln
        35           40           45
Val Gly Asp Lys Ala Leu Asp Phe Ser Leu Thr Thr Thr Asp Leu Ser
        50           55           60
Lys Lys Ser Leu Ala Asp Phe Asp Gly Lys Lys Lys Val Leu Ser Val
65           70           75           80
Val Pro Ser Ile Asp Thr Gly Ile Cys Ser Thr Gln Thr Arg Arg Phe
          85           90           95
Asn Glu Glu Leu Ala Gly Leu Asp Asn Thr Val Val Leu Thr Val Ser
        100          105          110
Met Asp Leu Pro Phe Ala Gln Lys Arg Trp Cys Gly Ala Glu Gly Leu
        115          120          125
Asp Asn Ala Ile Met Leu Ser Asp Tyr Phe Asp His Ser Phe Gly Arg
        130          135          140
Asp Tyr Ala Leu Leu Ile Asn Glu Trp His Leu Leu Ala Arg Ala Val
145          150          155          160
Phe Val Leu Asp Thr Asp Asn Thr Ile Arg Tyr Val Glu Tyr Val Asp
          165          170          175
Asn Ile Asn Ser Glu Pro Asn Phe Glu Ala Ala Ile Ala Ala Ala Lys
        180          185          190
Ala Leu

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Met Gly Tyr Arg Pro Ser Thr Ala Asn Ala Ile Ile His Gln Val Arg
 1             5             10             15
Glu Leu Leu Val Ser Arg Gly Tyr Thr Phe Tyr Asn Arg Lys Arg Leu
          20             25             30
Met Val Val Pro Lys Ser Val Val Lys Glu Leu Leu Gly Met Glu Leu
      35             40             45

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Met Gln Ala Val Glu His Phe Ile Lys Gln Phe Val Pro Glu His Tyr
 1             5             10             15
Asp Leu Phe Leu Asp Leu Ser Arg Glu Thr Lys Thr Phe Ser Gly Lys
          20             25             30
Val Thr Ile Thr Gly Gln Ala Gln Ser Asp Arg Ile Ser Leu His Gln
      35             40             45
Lys Asp Leu Glu Ile Thr Ser Val Glu Val Ala Gly Gln Ala Arg Pro
      50             55             60
Phe Thr Val Asp His Asp Asn Glu Ala Leu His Ile Glu Leu Ala Glu
      65             70             75             80
Ala Gly Gln Val Glu Leu Val Leu Ala Phe Ser Gly Lys Ile Thr Asp
          85             90             95
Asn Met Thr Gly Ile Tyr Pro Ser Tyr Tyr Thr Val Asp Gly Val Lys
          100             105             110
Lys Glu Val Leu Ser Thr Gln Phe Glu Ser His Phe Ala Arg Glu Ala
      115             120             125

```

Phe	Pro	Cys	Val	Asp	Glu	Pro	Glu	Ala	Lys	Ala	Thr	Phe	Asp	Leu	Ser
130						135					140				
Leu	Arg	Phe	Asp	Gln	Ala	Glu	Gly	Glu	Leu	Ala	Leu	Ser	Asn	Met	Pro
145				150					155					160	
Glu	Ile	Asp	Val	Glu	Asn	Arg	Lys	Glu	Thr	Gly	Ile	Trp	Lys	Phe	Glu
				165					170					175	
Thr	Thr	Pro	Arg	Met	Ser	Ser	Tyr	Leu	Leu	Ala	Phe	Val	Ala	Gly	Asp
			180					185					190		
Leu	Gln	Gly	Val	Thr	Ala	Lys	Thr	Lys	Asn	Gly	Thr	Leu	Val	Gly	Cys
		195					200					205			
Leu	Leu	Asn	Gln	Ser	Thr	Ser	Thr	Phe	Lys	Ser					
210						215									

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met	Ser	Gln	Glu	Phe	Leu	Ala	Arg	Ile	Leu	Glu	Gln	Lys	Ala	Arg	Glu
1				5					10					15	
Val	Glu	Gln	Met	Lys	Leu	Glu	Gln	Ile	Gln	Pro	Leu	Arg	Gln	Thr	Tyr
			20					25					30		
Arg	Leu	Ala	Glu	Phe	Leu	Lys	Asn	His	Gln	Asp	Arg	Leu	Gln	Val	Ile
		35					40					45			
Ala	Glu	Val	Lys	Lys	Ala	Ser	Pro	Ser	Phe	Gly	Glu	Ile	Ser	Ile	Ser
		50				55					60				
Met	Trp	Ile	Leu	Cys	Asn	Arg	Pro	Arg	Leu	Met	Lys	Lys	Thr	Glu	Gln
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

```

Met Ser Ser Phe Thr Pro Glu Asp Leu Gly Met Glu Gly Tyr Ala Met
 1           5           10           15
Glu Asp Ile Arg Gly Gly Asn Ala Gln Glu Asn Ala Glu Ile Leu Leu
      20           25           30
Ser Val Leu Lys Asn Glu Ala Ser Pro Phe Leu Glu Thr Thr Val Leu
      35           40           45
Asn Ala Gly Leu Gly Phe Tyr Ala Asn Gly Lys Ile Asp Ser Ile Lys
      50           55           60
Glu Gly Val Ala Leu Ala Arg Gln Val Ile Ala Arg Gly Lys Ala Leu
      65           70           75           80
Glu Lys Leu Arg Leu Leu Gln Glu Tyr Gln Lys
              85           90

```

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

```

Met Ile Tyr Thr Val Thr Leu Asn Pro Ser Ile Asp Tyr Ile Val Arg
 1           5           10           15
Leu Asp Gln Val Lys Val Gly Ser Val Asn Arg Met Asp Ser Asp Asp
      20           25           30
Lys Phe Ala Gly Gly Lys Gly Ile Asn Val Ser Arg Val Leu Lys Arg
      35           40           45
Leu Asn Ile Ser Asn Thr Ala Thr Gly Phe Ile Gly Gly Phe Thr Gly
      50           55           60
Lys Phe Xaa Xaa Asp Thr Leu Ala Glu Glu Glu Ile Glu Xaa Arg Phe
      65           70           75           80
Val Gln Val Ala Glu Asp Thr Arg Ile Asn Val Lys Ile Xaa Ala Asp
              85           90           95
Gln Glu Thr Glu Ile Asn Gly Thr Gly Pro Thr Val Glu Pro Val Lys
              100           105           110

```

```

Leu Glu Glu Leu Lys Ala Ile Leu Ser Ser Leu Thr Ala Glu Asp Thr
      115                      120                      125
Val Val Phe Ala Gly Ser Ser Ala Lys Asn Leu Gly Asn Val Ile Tyr
      130                      135                      140
Lys Gly Phe Asn Leu Leu Asp Ala Pro Asp Trp Cys Ala Ser Gly Leu
145                      150                      155                      160

```

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```

Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala Val
 1              5              10              15
Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala Val
      20              25              30
Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg Phe
      35              40              45
Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly Ala
 50              55              60
Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg Ser
65              70              75              80
Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln Val
      85              90              95
Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu Asn
      100             105             110
Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys Ala Ala Pro Tyr Pro
      115             120             125
Phe Gly Tyr Arg Lys
130

```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

Met Lys Ile Ile Ile Gln Arg Val Lys Lys Ala Gln Val Ser Ile Glu
 1             5             10             15
Gly Gln Ile Gln Gly Lys Ile Asn Gln Gly Leu Leu Leu Leu Val Gly
          20             25             30
Val Gly Pro Glu Asp Gln Glu Glu Asp Leu Asp Tyr Ala Val Arg Lys
          35             40             45
Leu Val Asn Met Arg Ile Phe Ser Asp Val Glu Gly Lys Met Asn Leu
          50             55             60
Ser Val Lys Asp Ile Glu Gly Glu Ile Leu Ser Ile Leu Ser Leu Pro
65             70             75             80
Leu Cys Gly Tyr

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Met Ile Lys Gly Thr Ile Lys Thr Val Ser Ile Met Ala Ala Thr Ser
 1             5             10             15
Gly Phe Leu Leu Tyr Asn Glu Val Phe Phe Leu Thr Asn Gly Ala Ala
          20             25             30
Gly Thr Lys Ser Ile Ser Phe Val Ile Arg Glu Leu Ala Val Ala Ser
          35             40             45
Ser Arg Thr Gln Tyr Ala Arg Ala Asn Thr Ile Gly Val Ile Gln Ile
          50             55             60
Leu Gly Gly Met Leu Ile Ile Val Cys Ile Asn Ile Leu Phe Arg Glu
65             70             75             80
Arg Lys Arg Leu Lys Gly Gly Lys
          85

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Met Gly Phe Gly Ile Pro Ala Ala Ile Gly Ala Lys Ile Ala Asn Pro
 1             5             10             15
Asp Lys Glu Val Val Leu Phe Val Gly Asp Gly Gly Phe Gln Met Thr
          20             25             30
Asn Gln Glu Leu Ala Ile Leu Asn Ile Tyr Lys Val Pro Ile Lys Val
          35             40             45
Val Met Leu Asn Asn His Ser Leu Gly Met Val Arg Gln Trp Gln Glu
          50             55             60
Ser Phe Tyr Glu Gly Arg Thr Ser Glu Ser Val Phe Asp Thr Leu Pro
65             70             75             80
Asp Phe Gln Leu Met Ala Gln Ala Tyr Gly Ile Lys Asn Tyr Lys Phe
          85             90             95
Asp Asn Pro Glu Thr Leu Ala Gln Asp Leu Glu Ala Thr Thr Glu Asp
          100            105            110
Val Pro Met Leu Ile Glu Val Asp Ile Ser Arg Lys Glu Gln Val Leu
          115            120            125
Pro Met Val Pro Ala Gly Lys Ser Asn His Glu Met Leu Gly Val Lys
          130            135            140
Phe His Ala
145

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met Trp Leu Pro Leu Asp Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly
 1             5             10             15
Ala Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu
          20             25             30
Thr Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile
          35             40             45
Thr Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Asn
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```

Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe Ser
 1             5             10             15
Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala Val
          20             25             30
Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
          35             40             45
Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
          50             55             60
Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
 65             70             75             80
Arg Asp Ile Pro Glu Leu Val Phe Trp Ile Val Leu Leu Asn Thr Arg
          85             90             95
Phe Trp Phe Ile Phe Ser Thr Thr Asn Ser Phe
          100             105

```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```

Met Lys Glu Ile Ile Glu Lys Leu Ala Lys Phe Glu Asn Leu Ser Gly
 1           5           10           15
Val Glu Met Thr Asp Val Ile Glu Arg Ile Val Thr Gly Arg Val Thr
      20           25           30
Glu Ala Gln Ile Ala Ser Leu Leu Leu Ala Leu Lys Met Lys Gly Glu
      35           40           45
Thr Pro Glu Glu Arg Thr Ala Ile Ala Gln Val Met Arg Gly His Ala
      50           55           60
Gln His Ile Pro Thr Glu Ile His Asp Ala Met Asp Asn Cys Gly Thr
      65           70           75           80
Gly Gly Asp Lys Ser Phe Ser Phe Asn Ile Ser Thr Thr Ala Ala Phe
      85           90           95
Val Leu Ala Gly Gly Gly Ile His Met Ala Lys His Gly Asn Arg Ser
      100           105           110
Ile Ser Ser Lys Ser Gly Ser Ala Asp Ser Xaa Asn Leu Gly Asn Gln
      115           120           125
Ser

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Met Asn Val Gln Met Ser Ser Lys Thr Asn Ile Leu Arg Ala His Ala
 1           5           10           15
Glu Met Gln Asn Ile Gln Arg Arg Ala Asn Glu Glu Arg Gln Asn Leu
      20           25           30
Gln Arg Tyr Arg Ser Gln Asp Leu Ala Lys Ala Ile Leu Pro Ser Leu
      35           40           45
Asp Asn Leu Glu Arg Ala Leu Ala Val Glu Gly Leu Thr Asp Asp Val
      50           55           60

```


(2) INFORMATION FOR SEQ ID NO:344:

(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

(2) INFORMATION FOR SEQ ID NO:345:

(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Met His Phe Asp Lys Ser Lys Phe Gly Ala Val Phe Ser Ala Pro Gly
 1             5             10             15
Leu Tyr Glu Val Glu Val Ile Asn Asn Ala Ser Phe Gly Gln Asn Ala
             20             25             30
Gln Tyr Glu Val Ile Gln Ser Arg Lys Leu Gly Thr Phe Ala Glu Leu
             35             40             45
Ile Glu Met Ala Lys Ile Lys
 50             55

```

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

Met Ile Gln Ala Val Phe Glu Arg Ala Glu Asp Gly Glu Leu Arg Ser
 1             5             10             15
Ala Glu Ile Thr Gly His Ala Glu Ser Gly Glu Tyr Gly Leu Asp Val
             20             25             30
Val Cys Ala Ser Val Ser Thr Leu Ala Ile Asn Phe Ile Asn Ser Ile
             35             40             45
Glu Lys Phe Ala Gly Tyr Glu Pro Ile Leu Glu Leu Asn Glu Asp Glu
             50             55             60
Gly Gly Tyr Leu Met Val Glu Ile Pro Lys Asp Leu Pro Ser His Gln
             65             70             75             80
Arg Glu Met Thr Gln Leu Phe Phe Glu Ser Phe Phe Leu Gly Met Ala
             85             90             95
Asn Leu Ser Glu Asn Ser Ser Glu Phe Val Gln Thr Arg Val Ile Thr
             100            105            110
Glu Asn

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

Met Thr Ala Ile Ser Met Lys Trp Leu Asn Asp Tyr Ile Trp Pro Ala
 1             5             10             15
Glu Ser Glu Phe Thr Pro Asp Met Thr Thr Asn Ala Val Lys Glu Ala
          20             25             30
Leu Thr Glu Met Leu Gln Ser Gly Thr Thr Thr Phe Asn Asp Met Tyr
          35             40             45
Asn Pro Asn Gly Val Asp Ile Gln Gln Ile Tyr Gln Val Val Lys Thr
          50             55             60
Ser Lys Met Arg Cys Tyr Phe Ser Pro Thr Leu Phe Ser Ser Glu Thr
65             70             75             80
Glu Thr Thr Ala Glu Thr Ile Ser Arg Thr Arg Ser Ile Ile Asp Glu
          85             90             95
Ile Leu Lys Tyr Lys Asn Pro Lys Phe Gln Gly Leu Trp
          100             105

```

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

```

Met Val Arg Glu Ser Ala Glu Ser Ala Gly Phe Phe Leu Glu Thr His
 1             5             10             15
Met Val Gln Gly Glu Trp Asn Thr Cys Val Phe Lys Lys Thr Lys Asp
          20             25             30
Ile Ser Gly Val Ile Gly Gly
          35

```

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
 1             5             10             15
Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
          20             25             30
Asn Gly Asn Ser Ser Lys His His Cys Arg Lys Cys Leu Gln Leu Gln
          35             40             45
Cys

```

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

Met Lys Ala Gln Leu Val Pro Ser Arg Ser Lys Tyr Leu Ile Asn Asp
 1             5             10             15
Asn Thr Val Val Leu Phe Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys
          20             25             30
Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg
          35             40             45
Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn Val Lys
          50             55             60
Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr Arg Val
        65             70             75             80
Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr Ser Leu
          85             90             95
Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr Val Asn
        100             105             110

```

Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Ala Val Asn Asn Glu Ile Gly Ser Ile Gln Xaa Ile Glu Ala Ile
 1 5 10 15
 Ser Glu Phe Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp Ala
 20 25 30
 Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu Arg
 35 40 45
 Val Asp Cys Ala Thr Phe Ser Ser His Lys Phe His Gly Val Arg Gly
 50 55 60
 Val Gly Phe Val Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu Leu
 65 70 75 80
 Thr Gly Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn Val
 85 90 95
 Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu Lys
 100 105 110
 Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile His
 115 120 125
 Gln Ala Leu Leu Asn Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu Glu
 130 135 140
 Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg Gly
 145 150 155 160
 Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser Thr
 165 170 175
 Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu Ile
 180 185 190
 Ala Met Gly Val Asp Lys Asp Lys Ala Lys Ser Ala Val Arg Leu Ser
 195 200 205
 Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr Lys
 210 215 220

Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
 225 230 235

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Leu Val Thr Gly Ala Ile Leu Gly Val Asn Val His Ile Phe Ser
 1 5 10 15
 Pro Lys Glu Leu Phe Pro Glu Lys Glu Ile Val Glu Leu Ala Glu Gly
 20 25 30
 Phe Ala Lys Glu Ser Gly Ala His Val Leu Ile Thr Glu Asp Ala Asp
 35 40 45
 Glu Ala Val Lys Asp Ala Asp Val Leu Tyr Thr Asp Val Trp Val Ser
 50 55 60
 Met Gly Glu Glu Asp Lys Phe Ala Glu Arg Val Ala Leu Leu Lys Pro
 65 70 75 80
 Tyr Gln Val Asn Met Asp Leu Val Lys Lys Ala Gly Asn Glu Asn Leu
 85 90 95
 Ile Phe Leu His Cys Leu Pro Ala Phe His Asp Thr His Thr Val Tyr
 100 105 110
 Gly Lys Asp Val Ala Glu Lys Phe Gly Val Glu Glu Met Glu Val Thr
 115 120 125
 Asp Glu Val Phe Arg Ser Lys Tyr Ala Arg His Phe Asp Gln Ala Glu
 130 135 140
 Asn Arg Met His Thr Ile Lys Ala Val Met Ala Ala Thr Leu Gly Asn
 145 150 155 160
 Leu Tyr Ile Pro Lys Val
 165

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Met Arg Leu Glu Gln Asp Cys Pro Val Phe Leu Lys Ile Lys Glu Lys
 1           5           10           15
Asp Met Ala Ser Lys Met Leu His Thr Cys Leu Arg Val Glu Asn Leu
          20           25           30
Glu Lys Ser Ile Ala Phe Tyr Gln Asp Ala Phe Gly Phe Lys Glu Leu
        35           40           45
Arg Arg Arg Asp Phe Pro Asp His Ala Phe Thr Ile Val Tyr Leu Gly
        50           55           60
Leu Glu Gly Asp Asp Tyr Glu Leu Glu Leu Thr Tyr Asn Tyr Asp His
65           70           75           80
Gly Pro Tyr Val Val Gly Asp Gly Phe Ala His Ile Ala Leu Ser Thr
          85           90           95
Pro Asp Leu Glu Ala Leu His Gln Glu His Ser Thr Lys Gly Tyr Glu
        100          105          110
Val Thr Glu Pro Asn Gly Leu Pro Gly Thr Ala Pro Asn Tyr Tyr Phe
        115          120          125
Val Lys Asp Pro Asp Gly Tyr Lys Val Glu Val Ile Arg Glu Lys
        130          135          140

```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```

Met Asp His Thr Ile Phe Cys Val Gly Tyr Arg Val Met Gln Lys Asp
 1           5           10           15
Leu Glu Gly Thr Leu Asp Ala Glu Lys Leu Lys Ala Ala Gly Val Pro
          20           25           30
Phe Gly Pro Leu Phe Gly Lys Ile Lys Asn Gly Gln Asp Leu Val Leu
        35           40           45

```

```

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
 50                      55                      60
Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
65                      70                      75                      80
Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
                      85                      90                      95
Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
                      100                     105                     110
Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
                      115                     120                     125
Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
                      130                     135                     140
Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
145                     150                     155                     160
Asp Leu Glu Lys Met Glu Ile Tyr Gln Ser Gln Lys Gly
                      165                     170

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Met Ile Gln Pro Ala Ser Leu Glu Glu Leu Ala Ser Leu Val Glu Lys
 1                      5                      10                      15
Ala Gly Lys Lys Val Phe Leu Phe Val Ala Asp Trp Cys Gly Asp Cys
                      20                      25                      30
Arg Tyr Ile Tyr Pro Ala Leu Pro Glu Ile Glu Glu Thr Asn Pro Glu
                      35                      40                      45
Phe Thr Phe Ile Arg Met Asp Arg Asp Gln Tyr Met Asp Leu Ala Lys
                      50                      55                      60
Leu Trp Asp Val Tyr Gly Ile Pro Ser Leu Val Val Leu Glu Lys Asp
65                      70                      75                      80
Lys Glu Ile Gly Arg Phe Val Asn Arg Asp Arg Lys Ser Lys Glu Gln
                      85                      90                      95
Ile Asn Asp Phe Leu Ala Gly Leu Lys
                      100                     105

```


(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Met Arg Leu Gly Leu Leu Gln Val Leu Arg Leu Pro Lys Ala Phe Gln
 1             5             10             15
Leu Ile Phe Ile Gln Asp Lys Gly His Gly Asp Val Ser Ser Phe Thr
          20             25             30
Ala Ser Cys Val Thr Gly Pro Trp Ala Phe Lys Leu Val Gly Lys Gln
          35             40             45
Gly Asn Ile His
          50

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

Met Lys Thr Arg Lys Ile Pro Leu Arg Lys Ser Val Val Ser Asn Glu
 1             5             10             15
Val Ile Asp Lys Arg Asp Leu Leu Arg Ile Val Lys Asn Lys Glu Gly
          20             25             30
Gln Val Phe Ile Asp Pro Thr Gly Lys Ala Asn Gly Arg Gly Ala Tyr
          35             40             45
Ile Lys Leu Asp Asn Ala Glu Ala Leu Glu Ala Lys Lys Lys Lys Val
          50             55             60
Phe Asn Arg Ser Phe Ser Met Glu Val Glu Ser Phe Tyr Asp Glu
          65             70             75             80

```

Leu Ile Ala Tyr Val Asp His Lys Val Lys Arg Arg Glu Leu Gly Leu
 85 90 95
 Glu

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met	Arg	Val	Ala	Tyr	Phe	Lys	Val	His	His	Pro	Ile	Tyr	Tyr	Tyr	Cys
1				5						10				15	
Ala	Tyr	Phe	Ser	Ile	Arg	Ala	Lys	Ala	Phe	Asp	Ile	Lys	Thr	Met	Gly
			20					25					30		
Ala	Gly	Leu	Glu	Val	Ile	Lys	Arg	Arg	Met	Glu	Glu	Ile	Ser	Glu	Lys
		35					40					45			
Arg	Lys	Asn	Asn	Glu	Ala	Ser	Asn	Val	Glu	Ile	Asp	Leu	Tyr	Thr	Thr
	50					55				60					
Leu	Glu	Ile	Val	Asn	Glu	Met	Trp	Glu	Arg	Gly	Phe	Lys	Phe	Gly	Lys
65				70					75					80	
Leu	Asp	Leu	Tyr	Cys	Ser	Gln	Thr	Thr	Glu	Phe	Leu	Ile	Asp	Gly	Asp
			85						90					95	
Thr	Leu	Ile	Pro	Pro	Phe	Val	Ala	Met	Asp	Gly	Leu	Gly	Glu	Asn	Val
			100					105					110		
Ala	Lys	Gln	Leu	Val	Arg	Ala	Arg	Glu	Glu	Gly	Glu	Phe	Leu	Ser	Lys
		115					120					125			
Thr	Glu	Leu	Arg	Lys	Arg	Gly	Gly	Leu	Ser	Ser	Thr	Leu	Val	Glu	Lys
	130					135					140				
Met	Asp	Glu	Met	Gly	Ile	Leu	Gly	Asn	Met	Pro	Glu	Ile	Thr	Ser	
145						150					155				

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

Met Ser Ser Lys Ile Ser Ile Gly Gln Leu Ile Thr Phe Asn Thr Leu
 1           5           10           15
Leu Ser Tyr Phe Thr Thr Pro Met Glu Asn Ile Ile Asn Leu Gln Thr
      20           25           30
Lys Leu Gln Ser Ala Lys Val Ala Asn Asn Arg Leu Asn Glu Val Tyr
      35           40           45
Leu Val Glu Ser Glu Phe Gln Val Gln Glu Asn Pro Val His Ser His
      50           55           60
Phe Leu Met Gly Asp Ile Glu Phe Asp Asp Leu Ser Tyr Lys Tyr Gly
      65           70           75           80
Phe Gly Arg Asp Thr Leu Thr Asp Ile Asn Leu Thr Ile Lys Gln Gly
      85           90           95
Asp Lys Val Ser Leu Val Gly Val Ser Gly Ser Gly Lys Thr Thr Leu
      100           105           110
Ala Lys Met Ile Val Asn Phe Phe Glu Pro Tyr Lys Gly His Ile Ser
      115           120           125
Ile Asn His Gln Asp Ile Lys Asn Ile Asp Lys Lys Ser Leu Ala Pro
      130           135           140
Ser Tyr
      145

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

Met Arg Gln Ala Pro Ala Leu Ala Gln Ala Asn Ile Glu Arg Val Val
 1           5           10           15
Val His Lys Ile Ser Lys Val Trp Glu Phe His Phe Arg Ile Phe
      20           25           30

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg
 1             5             10             15
Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp
      20             25             30
Tyr Tyr Leu Asp Gln Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn
      35             40             45
Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr
      50             55             60
Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp Gln Pro Asn
65             70             75             80
Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp Tyr Tyr
      85             90             95
Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp Gly Ser
      100            105            110
Thr Trp Tyr Tyr Leu Asn Ala Val Met Glu Ile
      115            120

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

Met Lys Trp Gly Ser Arg Ile Leu Leu Gly Leu Thr Pro Lys Ser Leu
 1             5             10             15

```

```

Arg Tyr Arg Ile Trp Lys Lys Ala Glu Lys Glu Met Thr Lys Tyr Asp
      20                      25                      30
Leu Ala Asp Cys Asp Gly Ile Thr Glu Leu Cys Ser Gly Pro Gly Tyr
      35                      40                      45
Met Arg Asn Lys Tyr Pro Ile Thr Ser Phe Glu Asp Asn Leu Phe Leu
      50                      55                      60
Pro Phe Glu Gly Thr Glu Met Pro Ile Pro Ile Gly Tyr Asp Val Tyr
      65                      70                      75                      80
Leu Arg Thr Ala Phe Gly Asp Tyr Met Thr Pro Pro Pro Ala Asp Lys
      85                      90                      95
Gln Val Pro His Gln Asp Ala Val Ile Ala Asp Met Asp Lys Ser Tyr
      100                     105                     110
Thr Glu Tyr Lys Gly Glu Tyr Gly Gly
      115                     120

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

Met Phe Pro Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile
  1                      5                      10                      15
Ala Leu Asp Asp Leu Phe Arg Ala Ala Ala Ile Tyr Ala Glu Ala Ile
      20                      25                      30
Tyr Glu Leu Ile Lys
      35

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

Met Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe Gln Asp
 1           5           10           15
Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr Leu Ser
           20           25           30
Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys Lys Ala
           35           40           45
Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly Gly His Ala Glu Ser Tyr
           50           55           60
Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu Ala Arg
65           70           75           80
Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro Thr Ser
           85           90           95
Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile Leu Gln
           100          105          110
Asn Arg Glu Leu Gly Met Thr His Ile Val Val Thr His Asp Leu Gln
           115          120          125
Phe Gly
           130

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

Met Tyr Gly Ala Asn Ser Glu Arg Leu Lys Glu Ser Leu Arg Ile Ser
 1           5           10           15
Leu Ser Pro Gln Asn Thr Val Glu Asp Leu Gln Thr Leu Ala Lys Thr
           20           25           30
Leu Lys Glu Ile Ile Gly Gly
           35

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
 1             5             10             15
Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
             20             25             30
Leu Glu His Tyr Ile Tyr Leu Leu Arg
             35             40

```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```

Met Lys His Phe Asp Thr Ile Val Ile Gly Gly Gly Pro Ala Gly Met
 1             5             10             15
Met Ala Thr Ile Ser Ser Ser Phe Tyr Gly Gln Lys Thr Leu Leu Ile
             20             25             30
Glu Lys Asn Arg Lys Leu Gly Lys Lys Leu Ala Gly Thr Gly Gly Gly
             35             40             45
Arg Cys Asn Val Thr Asn Asn Gly Ser Leu Asp Asn Leu Leu Ala Gly
             50             55             60
Ile Pro Gly Asn Gly Arg Phe Leu Tyr Ser Val Phe Ser Gln Phe Asp
             65             70             75             80
Asn His Asp Ile Ile Asn Phe Phe Thr Glu Asn Gly Val Lys Leu Lys
             85             90             95
Val Glu Asp His Gly Arg Val Phe Pro Ala Ser Asp Lys Ser Arg Thr
             100            105            110
Ile Ile Glu Ala Leu Glu Lys Lys Ile Thr Glu Leu Gly Gly Gln Val
             115            120            125

```

Ala Thr Pro Asn Arg Asn Arg Phe Cys
130 135

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met	Thr	Leu	Ala	Lys	Asp	Ile	Ala	Ser	His	Leu	Leu	Lys	Ile	Gln	Ala
1				5				10					15		
Val	Tyr	Leu	Lys	Pro	Glu	Glu	Pro	Phe	Thr	Trp	Ala	Ser	Gly	Ile	Lys
			20					25					30		
Ser	Pro	Ile	Tyr	Thr	Asp	Asn	Arg	Val	Thr	Leu	Ala	Tyr	Pro	Glu	Thr
			35				40						45		
Arg	Thr	Leu	Ile	Glu	Asn	Gly	Phe	Val	Glu	Ala	Ile	Lys	Glu	Ala	Phe
		50				55					60				
Pro	Glu	Val	Glu	Val	Ile	Ala	Gly	Thr	Ala	Thr	Ala	Gly	Ile	Pro	His
65					70					75				80	
Gly	Ala	Ile	Ile	Ala	Asp	Lys	Met	Asp	Leu	Pro	Phe	Ala	Tyr	Ile	Pro
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met	Val	Lys	Val	Leu	Ala	Ala	Cys	Gly	Asn	Gly	Met	Gly	Ser	Ser	Met
1				5				10					15		
Val	Ile	Lys	Met	Lys	Val	Glu	Asn	Ala	Leu	Arg	Lys	Leu	Asn	Gln	Thr
			20					25					30		


```

Asp Phe Thr Val Asn Ser Cys Ser Val Gly Glu Ala Lys Gly Leu Ala
   35                      40                      45
Val Gly Tyr Asp Ile Val Ile Ala Ser Leu His Leu Ile Gln Glu Leu
   50                      55                      60
Glu Gly Arg Thr Asn Gly Lys Leu Ile Gly Leu Asp Asn Leu Met Asp
   65                      70                      75                      80
Asp Lys Glu Ile Thr Glu Lys Leu Ser Gln Ala Ile Gln
                      85                      90

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

Met Ser Met Phe Leu Asp Thr Ala Lys Ile Lys Val Lys Ala Gly Asn
  1                      5                      10                      15
Gly Gly Asp Gly Met Val Ala Phe Arg Arg Glu Lys Tyr Val Pro Asn
                      20                      25                      30
Gly Gly Pro Trp Gly Gly Asp Gly Gly Arg Gly Gly Asn Val Val Phe
                      35                      40                      45
Val Val Asp Glu Gly Leu Arg Thr Leu Met Asp Phe Arg Tyr Asn Arg
                      50                      55                      60
His Phe Lys Ala Asp Ser Gly Glu Lys Gly Met Thr Lys Gly Met His
   65                      70                      75                      80
Gly Arg Gly Ala Glu Asp Leu Arg Val Arg Val Pro Gln Gly Thr Thr
                      85                      90                      95
Val Arg Asp Ala Glu Thr Gly Lys Val Leu Thr Asp Leu Ile Glu His
                      100                      105                      110
Gly Gln Glu Phe Ile Val Ala His Gly Gly Pro Trp Trp Thr Trp Lys
                      115                      120                      125
Tyr Ser Phe Arg Asp Thr Lys Lys Ser Cys Thr Gly Asn Leu
                      130                      135                      140

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A). LENGTH: 210 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Met Lys Gly Glu Met Thr Phe Lys Gln Val His Tyr Lys Tyr Gly
 1           5           10           15
Tyr Gly Arg Asp Val Leu Ser Asp Ile Asn Leu Thr Val Pro Gln Gly
          20           25           30
Ser Lys Val Ala Phe Val Gly Ile Ser Gly Ser Gly Lys Thr Thr Leu
          35           40           45
Ala Lys Met Met Val Asn Phe Tyr Asp Pro Ser Gln Gly Glu Ile Ser
          50           55           60
Leu Gly Gly Val Asn Leu Asn Gln Ile Asp Lys Lys Ala Leu Arg Gln
65           70           75           80
Tyr Ile Ile Tyr Leu Pro Pro Gln Pro Tyr Val Phe Asn Gly Thr Ile
          85           90           95
Leu Glu Asn Leu Leu Leu Gly Ala Lys Gly Gly Asp Asp Thr Gly Lys
          100          105          110
Ile Ser Leu Thr Gly Arg Ser Glu Phe Gly Ser Glu Ile Pro Lys Arg
          115          120          125
Asn Ile Ser Lys Pro Pro Cys His Leu Glu Ile Tyr Gln Thr Glu Leu
          130          135          140
Thr Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Arg Gln Arg Ile Ala
145          150          155          160
Leu Ala Arg Ala Leu Leu Thr Asp Ala Pro Val Leu Ile Leu Asp Glu
          165          170          175
Ala Thr Asn Ser Leu Asp Ile Leu Thr Lys Lys Arg Ile Val His Tyr
          180          185          190
Leu Met Ala Leu Asp Lys Thr Phe Asp Phe His Cys Ser Pro Leu Asp
          195          200          205
Tyr Cys
          210

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

Met Ala Arg Phe Ile Glu Ile Asp Ala Lys Glu His Asp Arg Val Thr
 1             5             10             15
Ser Gln Ile Ser His Phe Pro His Ile Leu Ala Ser Ser Leu Met Glu
             20             25             30
Gln Thr Ala Val Tyr Ala Gln Glu His Glu Asn Gly Lys Ala Leu Cys
             35             40             45
Gly Arg Trp Phe Ser Arg Tyr Asp Pro Asn Cys Gly Lys Arg Ala Arg
             50             55             60
Asn Val Asp Leu His Ser Leu Val Gln
65             70

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

Met Ala His Gln Gly Gln Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile
 1             5             10             15
Lys Glu Asp Asn Leu Glu Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe
             20             25             30
Ile Asn Leu His His Asn Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr
             35             40             45
Glu Asp Leu Cys Ala Ser Phe Gln Ala Ala Val Leu Asp Ile Leu Met
             50             55             60
Ala Lys Thr Lys Lys Ala Leu Glu Lys Tyr Pro Val Lys Thr Leu Val
65             70             75             80
Val Ala Gly Gly Val Ala Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala
             85             90             95
Ala Glu Val Thr Asp Val Lys Val Ile Ile Pro Pro Leu Arg Leu Cys
             100            105            110
Gly Asp Asn Ala Gly Met Ile Ala Tyr Ala Ser Val Ser Glu Trp Asn
             115            120            125

```

Lys Glu Asn Phe Ala Asn Leu Asp Leu Asn Ala Lys Pro Ser Leu Ala
 130 135 140
 Phe Asp Thr Met Glu
 145

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Lys Arg Ser Leu Asp Ser Arg Val Asp Tyr Ser Leu Leu Leu Pro
 1 5 10 15
 Val Phe Phe Leu Leu Val Ile Gly Val Val Ala Ile Tyr Ile Ala Val
 20 25 30
 Ser His Asp Tyr Pro Asn Asn Ile Leu Pro Ile Leu Gly Gln Gln Val
 35 40 45
 Ala Trp Ile Ala Leu Gly Leu Val Ile Gly Phe Val Val Met Leu Phe
 50 55 60
 Asn Thr Glu Phe Leu Trp Lys Val Thr Pro Phe Leu Tyr Ile Phe Arg
 65 70 75 80
 Leu Gly Thr Tyr Asp Leu Ala Asp Cys Ile Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe
 1 5 10 15

```

Leu Lys Asn Val Phe Glu Leu Glu Glu Glu Leu Glu Phe Gln Leu Leu
      20                      25                      30
Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro
      35                      40                      45
Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro
      50                      55                      60
Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu
      65                      70                      75                      80
Pro Glu Glu Asn Asp Leu Phe
                        85

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

Met Gly Lys Lys Asp Ala Ser Ala Met His Glu Met Arg Ala Ser Phe
  1                      5                      10                      15
Ile Gln Gly Ser Ile Glu Ala Gly His Thr Ala Glu Lys Ser Glu Gln
      20                      25                      30
Val Phe Asp Val Met Glu Lys Phe Ala Gly Tyr Gly Phe Asn Arg Ser
      35                      40                      45
His Ala Tyr Ala Tyr Ser Ala Leu Ala Phe Gln Leu Ala Tyr Phe Lys
      50                      55                      60
Thr His Tyr Pro Ala Ile Phe Tyr Gln Val Met Leu Asn Tyr Ser Asn
      65                      70                      75                      80
Ser Asp Tyr Leu Ile Asp Ala Leu Glu Ala Gly Phe Glu Val Ala Ser
      85                      90                      95
Leu Ser Ile Asn Thr Ile Pro Tyr His Asp Lys Ile Ala Asn Lys Ser
      100                      105                      110
Ile Tyr Ile Gly Leu Lys Ser Ile Lys Gly Leu Gln Gln Gly Leu Gly
      115                      120                      125
Ala Leu Asp Tyr
      130

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

Met Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr
 1             5             10             15
Glu Leu Asn Gln Ile Thr Gly Gly Glu Trp Trp Glu Glu Leu Leu His
             20             25             30
Glu Thr Ile Leu Ser Lys Phe Lys Ile Thr Lys Ala Leu Glu Leu Pro
             35             40             45
Ile Gln Leu
             50

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met Lys Lys Ala
 1             5             10             15
Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser
             20             25             30
Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr Met Gly Phe
             35             40             45
Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp
             50             55             60
Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr
             65             70             75             80
Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
             85             90

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

Met Leu Asn Glu Phe Pro Ile Phe Asp Tyr Glu Asp Ile Gln Leu Ile
 1             5             10             15
Pro Asn Lys Cys Val Ile Lys Ser Arg Ala Glu Ala Asp Thr Ser Val
          20             25             30
Thr Leu Gly Asn His Thr Phe Lys Leu Pro Val Val Pro Ala Asn Met
          35             40             45
Gln Thr Ile Leu Asp Glu Asn Val Ala Glu Gln Leu Ala Lys Gly Gly
          50             55             60
Tyr Leu Tyr Thr Tyr Ala Pro Phe
65             70

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

Met Asp Ile Lys Leu Lys Asp Phe Glu Gly Pro Leu Asp Leu Leu Leu
 1             5             10             15
His Leu Val Ser Lys Tyr Gln Met Asp Ile Tyr Asp Val Pro Ile Thr
          20             25             30
Glu Val Ile Glu Gln Tyr Leu Ala Tyr Val Ser Thr Leu Gln Ala Met
          35             40             45
Arg Leu Glu Val Thr Gly Glu Tyr Met Val Met Ala Ser Gln Leu Met
          50             55             60

```

(2) INFORMATION FOR SEQ ID NO:381:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

(2) INFORMATION FOR SEQ ID NO:382:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile Val Glu Pro Val Leu
 1             5             10             15
Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu Glu Glu Lys Ala Thr
          20             25             30
Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln Asn Asp Leu Ala Glu
          35             40             45
Leu Lys Asn
          50

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
 1             5             10             15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
          20             25             30
Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
          35             40             45
Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
          50             55             60
Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
          65             70             75             80
Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
          85             90             95
Ile Lys Gly Xaa Ser Thr Leu Thr Phe Ile Ile Gly Gly Ser Leu Gly
          100             105             110
Leu Ser Ser Ser Val Lys Asn Arg Ala Asn Leu Ser Val Ser Phe Gly
          115             120             125

```

Arg Leu Thr Leu Pro His Gln Leu Met Arg Leu Val Leu Val Glu Gln
 130 135 140
 Ile Tyr Arg Ala Phe Thr Ile Gln Gln Gly Phe Pro Tyr His Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Gly Ile Leu Ala Trp Cys Asp Leu Val Leu Tyr Arg Leu Trp Asp
 1 5 10 15
 Ser Phe Met Asp Leu Gly Leu Phe Ile Asn Asp Ala Trp Val Arg Lys
 20 25 30
 Lys Lys Thr Leu Asn Lys Glu Arg Lys Lys Ala Gly Lys Ala Ala Leu
 35 40 45
 Pro Glu Asn Arg Trp Ile Gln Leu Leu Gly Met Val Val Thr Phe His
 50 55 60
 Val Val Met Leu Ser Phe Leu Ile Phe Ser Gly Phe Leu Asn Asn Leu
 65 70 75 80
 Trp Phe Lys Lys

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Val Met Ala Glu Asp Gln Ala Val Arg Gln Asn Arg Leu Ala Ile
 1 5 10 15

Leu Ser Gln Leu Thr Lys Lys Ala Ala Lys Phe Ala Cys Phe Asn Gln
 20 25 30
 Ile Asn Thr Lys
 35

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Gly Ala Gln Pro Val Gln Asp Thr Glu Thr Ser Ser Ala Leu Ile
 1 5 10 15
 Ser Ser His Tyr Leu Asp Glu Gln Asp Leu Ser Glu Lys Leu Lys Ser
 20 25 30
 Glu Leu Gln Trp Phe Glu Leu Glu Asn Lys Leu Leu Asn Leu Trp Glu
 35 40 45
 His

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Asp Glu Val Thr Ile Phe Gly Ile Asn Tyr Phe Lys Glu His Tyr
 1 5 10 15
 Pro Glu Lys Leu Ala Glu Arg Phe Lys Gln Met Lys Ile Glu Glu Glu
 20 25 30
 Ala Pro Val Ile Ile Met Asp Met Thr Arg Ala Leu Gly Phe Arg Asp
 35 40 45

Asp Tyr Asp Arg Phe Tyr Ser Leu Phe Arg Glu Gly Ser Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
 1 5 10 15
 Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Xaa Leu Leu Leu Leu Gly
 20 25 30
 Gly Thr Tyr Pro Tyr Gly Val Xaa Ser Ser Trp Leu Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
 1 5 10 15
 Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
 20 25 30
 Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
 35 40 45
 Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
 50 55 60
 Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
 65 70 75 80

```

Val Leu Ile Leu Ala Leu Asn Cys Tyr Gln His Cys Leu Glu His Ser
      85                      90                      95
Ser Phe Tyr Asn Ala Asn Tyr Phe Glu Ala Tyr Thr Glu Lys Ile Ile
      100                    105                    110
Asp Lys Gly Ile Lys Leu Tyr Glu Arg Asn Val Phe His Tyr Leu Lys
      115                    120                    125
Gly Phe Ala Leu Tyr Gln Lys Gly Gln Cys Lys Glu Gly Cys Lys Gln
      130                    135                    140
Met Gln Glu Thr Met His Ile Phe Asp Val Leu Gly Leu Pro Glu Gln
      145                    150                    155                    160
Val Ser Leu Leu Ser Gly Thr Leu Arg Lys Ile Cys Gln Lys Leu Ile
      165                    170                    175
Phe Pro Asn Lys Gly Lys Asn Lys Lys Leu Leu Ser Val Leu Ile Gln
      180                    185                    190

```

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Ser Thr Val Leu Ser Trp Thr Ala Tyr Lys Thr Gln Arg Leu Glu
 1              5              10              15
Met Ser Ile Leu Leu His Met Ile Val Asn Gly Ile Ala Phe Cys Leu
      20              25              30
Leu Ala Leu Val Val Ile Met Ser Arg Thr Leu Gly Ile Ser Val
      35              40              45

```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

Met Arg Glu Asn Asp Leu Leu Leu Ile Thr Ala Asp His Gly Asn Asp
 1             5             10             15
Pro Thr Tyr Ala Gly Thr Asp His Thr Arg Glu Tyr Ile Pro Leu Leu
          20             25             30
Ala Tyr Ser Pro Ala Phe Lys Gly Asn Gly Leu Ile Pro Val Gly His
          35             40             45
Phe Ala Asp Ile Ser Ala Thr Val Ala Asp Asn Phe Gly Val Glu Thr
          50             55             60
Ala Met Ile Gly Glu Ser Phe Leu Asp Lys Leu Val
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser Leu Leu Gly Gly
 1             5             10             15
Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala Ala Lys His Ala
          20             25             30
Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr Glu Lys Asp Ala
          35             40             45
Thr Pro Pro Val Glu Ile Ala Ser Ile Thr Lys Leu Ile Thr Val Tyr
          50             55             60
Leu Val Tyr Glu Ala Leu Glu Asn Gly Ser Ile Thr Leu Ser Thr Pro
65             70             75             80
Val Asp Ile Ser Asp Tyr Pro Tyr Gln Leu Thr Thr Asn Ser Glu Ala
          85             90             95
Ser Asn Ile Pro Met Glu Ala Arg Asn Tyr Thr Val Glu Glu Leu Leu
          100             105             110
Glu Ala Thr Leu Val Ser Ser Ala Asn Ser Ala Ala Ile Ala Leu Ala
          115             120             125
Glu Lys Ile Ala Gly Ser Glu Lys Asp Phe Val Xaa Met Met Arg Ala
          130             135             140

```

Lys Leu Leu Glu Trp Gly Ile Arg Ile His Cys Cys Gln Tyr Asp Arg
 145 150 155 160
 Ser

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Ser Asn Ala Met Glu Gly Val Leu Tyr Phe Leu Lys Pro Asp Phe
 1 5 10 15
 Ser Lys Leu Thr Ser Ala Asp Leu Leu Tyr Ala Leu Gly Gln Ser Phe
 20 25 30
 Phe Ala Leu Ser Leu Gly Val Thr Asp Met Leu Thr Tyr Ala Ser Tyr
 35 40 45
 Leu Asp Lys Lys Thr Asn Leu Val Gln Ser Gly Ile Ser Ile Val Thr
 50 55 60
 Met Asn Ile Ser Ile Val His His Gly Arg Ser Ser His Phe Pro Ser
 65 70 75 80
 His Val Ser Leu Gln Tyr Pro Leu
 85

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Lys Val Ala Lys Pro Phe Trp Ala Ile Val Lys Leu Lys Ser Val
 1 5 10 15

Gln His Ala Ser Met Leu Glu Asn Pro Lys Glu Met Asp Gly Leu Met
 20 25 30
 Lys Gln Val Glu Asn Leu Ala Leu Glu Asn Gln Gly Tyr Gln Val Glu
 35 40 45
 Lys Glu Asn Lys Ala Phe Glu Gln Ile Lys Asp Ser Val Ala Thr Phe
 50 55 60
 Gln Thr Phe Leu Thr Ile Phe Leu Tyr Gly Cys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met Asp Ala Glu Val Ser Lys Asn Leu Arg Leu Ile Leu Glu Arg Lys
 1 5 10 15
 Gly Met Thr Ile Leu Thr Gly Thr Lys Leu Gln Glu Ile Ile Glu Glu
 20 25 30
 Asn Gly Gln Leu Arg Ile Lys Val Glu Gly Lys Asp Asn Ile Ile Ala
 35 40 45
 Ser Lys Ala Leu Leu Ser Ile Gly Arg Met Pro Asp Leu Glu Gly Ile
 50 55 60
 Gly Glu Val Glu Phe Glu Leu Asp Arg Gly Cys Ile Lys Val Asn Glu
 65 70 75 80
 Tyr Met Glu Thr Ser Val Pro Arg Ile Tyr Ala Thr Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Met Lys Asn Ser Ile Met Asp Thr Lys Phe Asp Arg Arg Ile Leu Leu
 1           5           10           15
Leu Asn Lys Ile Ile Ile Val Phe Ile Val Leu Met Thr Leu Leu Pro
           20           25           30
Leu Leu Tyr Ile Val Val Ala Ser Phe Met Asp Pro Lys Val Leu Val
           35           40           45
Ser Arg Gly Ile Ser Phe Asn Pro Ala Asp Trp Thr Val Glu Gly Tyr
           50           55           60
Gln Arg Val Ile Gln
65

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```

Met Val Ile Pro Glu Ala Gly Tyr Leu Tyr Ala Phe His Tyr Pro Asn
 1           5           10           15
Leu Lys Gly Lys Gly Lys Glu Ala Val Gln Val Ile Tyr Asn Leu Asn
           20           25           30
Leu Ala Ser Ala Lys Val Ile Gln Leu Tyr Arg Ser Leu Gly Leu Asp
           35           40           45
Gly Lys Ile Gly Ile Ile Leu Asn Leu Thr Pro Ala Tyr Pro Arg Ser
           50           55           60
Asn Ser Pro Glu Asp Leu Glu Ala Ser Arg Phe Thr Asp Asp Phe Phe
65           70           75           80
Asn Lys Val Phe Leu Glu Ser Ser Cys
85

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

Met Thr Arg Ile Ala Ser Val Ser Val Ile Arg Asn Ala Ala Phe Ile
 1           5           10           15
Ala Ile Ala Leu Ser Phe Leu Gly Lys Phe Thr Ala Leu Ile Ser Thr
      20           25           30
Ile Pro Asn Ala Val Leu Gly Gly Met Ser Ile Leu Leu Tyr Gly Val
      35           40           45
Ile Ala Ser Asn Gly Leu Lys Val Leu Ile Lys Glu Arg Val Asp Phe
      50           55           60
Ala Gln Met Arg Asn Leu Ile Ile Ala Ser Ala Met Leu Val Leu Gly
65           70           75           80
Leu Gly Arg Ser Tyr Pro
      85

```

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

Met Ser Leu Arg Glu Lys Ser Met Ser Glu Tyr Lys Leu Ser Glu Asn
 1           5           10           15
Asn Trp Thr Arg Val Ala Val Phe Ala Gly Gly Asn Arg Gly His Tyr
      20           25           30
Arg Thr Asp Phe Asp Ala Phe Val Gly Val Asp Arg Gly Ser Leu Trp
      35           40           45
Val Leu Glu Glu Asp Leu Pro Leu Ala Leu Ala Val Gly Asp Phe Asp
      50           55           60
Ser Val Thr Glu Glu Glu Arg Gln Val Ile Gln Lys Arg Ala Gln Tyr
65           70           75           80
Phe Val Gln Ala Arg Pro Glu Lys Asp Asp Thr Asp Leu Glu Leu Ala
      85           90           95

```

Leu Leu Thr Ile Phe Glu Gln Asn Pro Gln Ala Glu Val Thr Ile Phe
 100 105 110
 Gly Ala Leu Gly Gly Arg Ile Asp His Met Leu Ala Asn Val Leu Ser
 115 120 125
 Thr

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
 1 5 10 15
 Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
 20 25 30
 Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
 35 40 45
 Asp Ser Ala Asp Asn Leu Leu Val Asn His
 50 55

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Ile Tyr Gly Ala Ile Ile Asp Ala Lys Thr Ala Glu Asn Ala Ala
 1 5 10 15
 Gly Met Thr Ala Met Gln Thr Ala Thr Asp Asn Ala Lys Lys Val Ile
 20 25 30

Asn Asp Leu Thr Ile Gln Tyr Asn Arg Ala Gln Thr Gly Gly Tyr Tyr
 35 40 45
 Thr Arg Asn Tyr Arg Asn Arg Ser Ser Ala
 50 55

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Thr Asp Gly Tyr Glu His Tyr Lys Lys Ile Met Glu Asn Pro Pro
 1 5 10 15
 Lys Asn Leu Ile Phe Pro Gly Ile Val Ser Pro Glu Arg Met Arg Glu
 20 25 30
 Ile Val Cys Ser Asn Gly Ser Phe Leu Val Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ser Lys Gln Lys Lys Phe Glu Glu Asn Leu Ala Glu Leu Glu Thr
 1 5 10 15
 Ile Val Gln Ser Leu Glu Asn Gly Glu Ile Ala Leu Glu Asp Ala Ile
 20 25 30
 Thr Ala Phe Gln Lys Gly Met Val Leu Ser Lys Glu Leu Gln Ala Thr
 35 40 45
 Leu Asp Lys Ala Glu Lys Thr Leu Val Lys Val Met Gln Glu Asp Gly
 50 55 60

Thr Glu Ser Asp Phe Glu
65 70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

Met Phe Ala Ala Val Thr Ala Gly Tyr Gln Ala Ala Leu Met Val Pro
 1           5           10           15
Thr Glu Ile Leu Ala Glu Gln His Phe Glu Ser Leu Gln Asn Leu Phe
      20           25           30
Pro Asn Leu Lys Leu Ala Leu Leu Thr Gly Ser Leu Lys Ala Ala Glu
      35           40           45
Lys Arg Glu Val Leu Glu Thr Ile Ala Lys Gly Glu Ala Asp Leu Ile
      50           55           60
Ile Gly Thr His Ala Leu Ile Gln Asp Gly Val Glu Tyr Ala Arg Leu
65           70           75           80
Gly Leu Ile Ile Ile Asp Glu Gln His Arg Phe Gly Val Gly Gln Arg
      85           90           95
Arg Ile Leu Arg Glu Lys Gly Asp Asn Pro Asp Val Leu Met Met Thr
      100          105          110
Ala Thr Pro Ile Pro Arg Thr Leu Ala Ile Thr Ala Phe Gly Asp Met
      115          120          125
Asp Val Ser Ile Ile Asp Gln Met Pro Ala Gly Arg Lys Pro Tyr Cys
      130          135          140
Asp Ala Leu Asp Gln Thr
145          150

```

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

Met Asn Arg Glu Ala Leu Arg Leu Tyr Leu Val Thr Asn Arg Tyr Gln
 1             5             10             15
Asp Ser Val Glu Ser Phe Leu Ala Lys Val Glu Thr Ala Cys Arg Ser
          20             25             30
Gly Val Thr Ile Val Gln Leu Arg Glu Lys Asn Leu Thr Thr Asn Gln
          35             40             45
Tyr Tyr Gln Leu Ala Lys Gln Val Lys Glu Ile Thr Asp Ala Tyr Gln
          50             55             60
Val Pro Leu Ile Ile Asp Asp Arg Leu Asp Val Cys Leu Ala Val Asp
65             70             75             80
Ala Ala Gly Leu His Ile Gly Asp Asp Glu Leu Pro Val Ser Val Ala
          85             90             95
Arg Gln Val Leu Gly Pro Glu Lys Ile Pro Arg Cys His Arg
          100             105             110

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

Met Gln Gly Ser His Phe His Leu Pro Ile Tyr Arg Met Thr Ser Gln
 1             5             10             15
Ala Leu Leu Asp Glu Thr Lys Lys Val Ala Ile Pro Val Leu Ala Thr
          20             25             30
Thr Gln Ser Lys Asp Ser Val Asp Tyr Arg Glu Leu Pro Ser Ile Glu
          35             40             45
Asn Phe Val Leu Val Met Gly Asn Glu Gly Gln Gly Ile Ser Pro Leu
          50             55             60
Met Ala Glu Ser Ala Asp Gln Leu Val His Ile Ser Met Lys Gly Gln
65             70             75             80
Ala Glu Ser Leu Asn Val Ala Val Ala Ala Gly Ile Leu Ile Phe His
          85             90             95
Leu Ser

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

Met Thr Lys Thr Ala Phe Leu Phe Ala Gly Gln Gly Ala Gln Tyr Leu
 1             5             10             15
Arg Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr
      20             25             30
Ile Asp Arg Ala Ser Gln Val Leu Gly Tyr Asp Leu Arg Tyr Leu Ile
      35             40             45
Asp Thr Glu Glu Asp Lys Leu Asn Gln Thr Arg Tyr Thr Gln Pro Ala
      50             55             60
Ile Leu Ala Thr Ser Val Ala Ile Tyr Arg Leu Leu Gln Glu Lys Gly
65             70             75             80
Tyr His Pro Asp Met Val Ala Gly Leu Ser Leu Gly Glu Tyr Ser Ala
      85             90             95
Leu Val Ala Ser Gly Ala Leu Asp Phe Glu Asp Ala Val Ala Leu Val
      100            105            110
Ala Lys Arg Gly Ala Tyr Met Glu Glu Ala Ala Pro Ala Asp Ser Gly
      115            120            125
Lys Met Val Ala Val Leu His Thr Pro
      130            135

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
 1           5           10           15
Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
          20           25           30
Leu

```

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

```

Met Thr Lys Glu Thr Gly Met Glu Gln Thr Phe Phe Ile Ile Lys Pro
 1           5           10           15
Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val Leu Lys Arg Ile Glu
          20           25           30
Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe Arg Ser Gln Val Phe
          35           40           45
Arg Arg Val Asp
          50

```

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```

Met Thr Ser Gly Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val
 1           5           10           15

```


Ile Glu Thr Trp Arg Thr Met Met Gly Ala Thr Arg Pro Glu Glu Ala
 20 25 30
 Leu Pro Gly Thr Ile Arg Gly Asp Phe Ala Lys Ala Ala Gly Glu Asn
 35 40 45
 Glu Ile Ile Gln Asn Val Val His Gly Ser Asp Ser Glu Lys Asn Gln
 50 55 60
 Leu Ser Arg Glu Ile Ala Pro Leu Val Leu Arg Val Asp Trp Leu Asn
 65 70 75 80
 Gln Leu Asp Lys Ser Ser Phe Glu
 85

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Gly Leu Lys Asp Asn Ala Gly Leu Val Lys Glu Tyr Ala Leu Val
 1 5 10 15
 Asp Ala Val Glu Tyr Gln Asn Val Ile Val Ala Thr Thr Val Glu Glu
 20 25 30
 Met Leu Ser Lys Tyr Ala Asn Lys Asn Asp Leu Glu Ile Asp Asn Ala
 35 40 45
 Thr Thr Glu Ser Ile Lys Gly Val Val Ala Asp Leu Lys Ser Ala Val
 50 55 60
 Ile Lys Gly Asp Thr Val Tyr Phe Phe Lys Val Asp Gly Lys Ile Tyr
 65 70 75 80
 Lys Val Lys Ala Ser Val Ser Asp Asp Leu Pro Tyr Leu Glu Asn Gly
 85 90 95
 Lys Thr Phe Glu Gly Gln Val Xaa Lys Asp Asn Tyr Leu Lys Thr Phe
 100 105 110
 Lys Val Gln
 115

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

Met Ile Ser Gly Ser Glu Ile Arg Asp Ile Val Thr Ser Asp Ile Pro
 1             5             10             15
Leu Ala Asp Lys Thr Glu Thr Leu Val Arg Phe Ala Asn Asn Ala Gly
          20             25             30
Gly Leu Asp Asn Ile Thr Val Ala Leu Val Ser Met Asn Glu Glu Asp
          35             40             45
Glu Glu
          50

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
 1             5             10             15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
          20             25             30
Met Val Glu Ala Asn Arg Leu Ser Ser Met Ile Leu Tyr Gly Pro Pro
          35             40             45
Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
          50             55             60
Tyr Ala Phe Arg Thr Phe Asn Ala Thr Val Asp Ser
          65             70             75

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Ala Gln
 1             5             10             15
Glu Gln Val Val Leu Gly Asn Thr Tyr His Thr Gly Asn His Cys Phe
          20             25             30
Ser

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp Val Ile Asp Ala
 1             5             10             15
Gly His Val Thr Gly Phe Leu Tyr Thr Val His Ser Ser Ser Thr Gly
          20             25             30
Leu Ile Val Leu Gln Ile Lys Lys Asp Leu Leu Lys Leu
          35             40             45

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

Met Thr Asp Arg Tyr Asp Ser Ser Leu Gly Ile Tyr Lys Val Pro Trp
 1           5           10           15
Cys Val Ser Gln Gln Gln Thr Val Thr Glu Ile Met Asp Thr Tyr Cys
          20           25           30
Asp Trp Gly Val Lys Tyr Pro Leu Val Tyr Leu Glu Asp Pro Phe Ser
          35           40           45
Asp Glu Asp Leu Asp Ser Trp Arg Lys Phe Gln Leu Ile Lys Pro Leu
          50           55           60
Lys Leu Gln Val Phe Gly Asp Asp Phe Tyr Ala Thr Asn Leu Glu Arg
65           70           75           80
Ile Ser Gln Phe Lys Asp Cys Ala Asp Gly Ile Val Ile Lys Pro Asn
          85           90           95
Gln Val Gly Ser Val Ser Lys Thr Leu Glu Val Met Glu Tyr Ala Glu
          100          105          110
Lys Ser Gly Ile Ser Met Ala Phe Ser Gln Arg Thr Ala Glu Thr Glu
          115          120          125
Asn Asn Ile Ile Ser His Leu Ala Met Ser Val Ile Leu Leu Ile
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

Met Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
 1           5           10           15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
          20           25           30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
          35           40           45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
          50           55           60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
65           70           75           80

```

Gly Leu Ala Pro Tyr Phe Asn Gln Val Phe Ile Ser Glu Gln Leu Gln
 85 90 95
 Thr Gln Lys Pro Asp Ala Leu Phe Tyr Glu Lys Ile Gly Gln Gln Ile
 100 105 110
 Ala Gly Phe Ser Lys Glu Lys Thr
 115 120

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met His Arg Lys Thr Val Ile Asp Xaa Arg Thr Leu Gly Glu Arg Tyr
 1 5 10 15
 Thr Phe Thr Xaa Pro Ile Lys Glu Leu Lys Thr Arg Asn Val Ala Glu
 20 25 30
 Val Ala Asp Leu Leu Ala Xaa Val Glu Ser Tyr Gln Glu Gln Asp Tyr
 35 40 45
 Tyr Val Val Gly Tyr Val Ser Tyr Glu Ala Ala Pro Ala Phe Glu Glu
 50 55 60
 Lys Leu Ala Val His Lys Val Pro Leu Leu Gly Glu Tyr Leu Leu Tyr
 65 70 75 80
 Phe Thr Val His Asp Arg Val Glu Thr Ser Pro Ile Pro Leu Thr Tyr
 85 90 95
 Glu Asp Ile Asp Leu Pro Ser Asn Trp Gln Gly Xaa Asn Val Cys Thr
 100 105 110
 Glu Leu

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

Met Glu Arg Ile Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly
 1             5             10             15
His Val Phe Thr Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys
             20             25             30
Ile Asn Ser Ala Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys
             35             40             45
Ala Gly Tyr Gly Tyr Leu Leu Pro Tyr Leu Asn Lys
             50             55             60

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

```

Met Glu Trp Ile Arg Leu Ile Gly Ile Ala Ile Ile Val Val Gly Phe
 1             5             10             15
Ile Leu Lys Phe Asp Thr Ile Ala Thr Val Val Leu Ala Gly Leu Val
             20             25             30
Thr Ala Leu Val Ser Gly Val Ser Leu Val Glu Phe Leu Glu Ile Leu
             35             40             45
Gly Lys Glu Phe Ser Asn Gln Arg Val Leu Thr Ile Phe Met Val Thr
             50             55             60
Leu Pro Leu Val Gly Leu Ser Glu Thr Phe Gly Leu Asn Asn Asp Gln
             65             70             75             80
Ser Ile

```

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

```

Met Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
 1             5             10             15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
      20             25             30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
      35             40             45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
      50             55             60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Arg Leu Phe Leu Arg Ala
65             70             75             80
Pro Ile Ile Val Phe Gly Ala Ile Phe Met Ala Tyr Arg Ile Ser Ala
      85             90             95
Glu Leu Thr Phe Trp Phe Leu Val Met Val Ala Ile Leu Thr Ile Val
      100            105            110
Ile Val Arg Val Ile Ser Ile Gly Gln Ser Ser Leu Gln
      115            120            125

```

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```

Met Pro Ile Glu Gln Val Gln Lys Leu Leu Gly His Ser Lys Ile Asp
 1             5             10             15
Thr Thr Leu Ala Tyr Ala Met Val Asn Gln Asn Asn Val Lys His Ser
      20             25             30
His Gln Lys Phe Ile Ser
      35

```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```

Met Lys Pro Cys Trp Lys Lys Cys Phe Pro Glu Glu Val Ser Ser Glu
 1             5             10             15
Gly Glu Val Thr Leu Ile Glu Ile Pro Val Ser Asp Lys Ile Ala Gly
          20             25             30
Lys Gln Val His Glu Leu Asn Leu Pro His Asn Val Leu Ile Thr Thr
          35             40             45
Gln Val His Asn Gly Lys Ser Gln Thr Val Asn Gly Ser Thr Arg Met
 50             55             60
Tyr Leu Gly Asp Met Ile His Leu Val Ile Pro Lys Ser Glu Ile Gly
65             70             75             80
Lys Val Lys Asp Leu Leu Leu
          85

```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Asn Glu Gly Val Glu Asn Phe Arg Ala Lys Leu Ala Ser Leu Gly
 1             5             10             15
Ala Lys Asn Ile Gly Ile Tyr Val Gly Val Tyr Phe Met Glu Glu His
          20             25             30
Ser Ile Asp Thr Gly Lys Phe Thr Ser Val Trp Ile Pro Ser Tyr Gly
          35             40             45
Ser Asp Ser Gly Phe Leu Glu Ser Ser Pro Lys Thr Asp Leu Asp Tyr
50             55             60

```


(2) INFORMATION FOR SEO ID NO:425:

(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

(2) INFORMATION FOR SEQ ID NO:426:

(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Met Glu Asp Xaa Glu Thr Gln Arg Val Val Met Gln Tyr Arg Ala Pro
 1           5           10           15
Glu Asn Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly His Val Glu
          20           25           30
Asn Asp Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile Tyr Glu Glu
          35           40           45
Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Ile Lys Asn Trp
          50           55           60
Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Ile Cys Tyr Lys Ala Thr
65           70           75           80
Glu Phe Ser Gly Thr Leu Gln Ser Ser Glu Glu Gly Glu Val Ser Trp
          85           90           95
Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr Asp Met Leu
          100          105          110
Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu Phe Phe Tyr
          115          120          125
Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
 1           5           10           15
Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
          20           25           30
Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
          35           40           45
Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
          50           55           60
Pro His Val
65

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```

Met Lys Lys Leu Val Phe Val Cys Leu Gly Asn Ile Cys Arg Ser Pro
 1           5           10           15
Met Ala Glu Phe Val Met Lys Ser Met Thr Asp Asn Tyr Glu Ile Gln
          20           25           30
Ser Arg Ala Thr Ser Ser Trp Glu His Gly Asn Pro Ile His Lys Gly
          35           40           45
Thr Gln Gly Ile Phe Gln Glu Tyr Glu Ile Pro Tyr Asp Lys Asn Lys
          50           55           60
Thr Ser Leu Gln Ile Ser Lys Glu Asp Phe Glu Ala Phe Asp Tyr Ile
          65           70           75           80
Ile Gly Met Asp Ala Ser Asn Val Pro Thr Tyr Val Arg Cys Val Gln
          85           90           95

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

Met Val Lys Tyr Gly Val Val Gly Ala Gly Tyr Phe Gly Ala Glu Leu
 1           5           10           15
Ala Arg Tyr Met Gln Lys Asn Asp Gly Ala Xaa Ile Thr Leu Leu Tyr
          20           25           30
Asp Pro Asp Asn Ala Glu Ala Ile Ala Glu Glu Leu Gly Ala Lys Val
          35           40           45
Ser Lys Phe Leu Arg
          50

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

Met Leu Trp Lys Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His
 1             5             10             15
Leu Thr Thr Glu Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu
          20             25             30
Lys Gln Ala Lys Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg
      35             40             45
Glu Gly Asn Pro Phe Val Thr Ala Lys Asn Leu Lys Gln Ser Ala Leu
      50             55             60
Thr Gln Cys Glu Val Xaa Leu Asn Leu Leu
65             70

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

Met Asn Thr Leu Tyr Leu Asn Gln His Ser Ser Tyr Lys Asn Asp Glu
 1             5             10             15
Asp Ser His Ser Phe Pro Ile Gln Met Glu Leu Val Ser Asp Glu Met
          20             25             30
Ile Pro Arg Asn
      35

```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Met Ala Arg Lys Glu Thr Met Ala Glu Arg Lys Tyr Cys Lys Met Lys
 1             5             10             15
Lys Asp Ile His Pro Glu Tyr Arg Pro Val Val Phe Met Asp Thr Thr
             20             25             30
Thr Gly Tyr Gln Phe Leu Ser Gly Ser Thr Lys Arg Ser Asn Glu Thr
             35             40             45
Val Glu Phe Glu Gly Glu Thr Tyr Pro Leu Ile Arg Val Glu Ile Ser
             50             55             60
Ser Asp Ser His Pro Phe Tyr Thr Gly Arg Gln Lys Phe Thr Gln Ala
65             70             75             80
Asp Gly Arg Val Asp Arg Phe Asn Lys Lys Tyr Gly Leu Lys
             85             90

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr Asn Val Ala
 1             5             10             15
Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln Thr Tyr Gln
             20             25             30
Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp Glu Ser Gly
             35             40             45
Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val Ser Val Leu
50             55             60

```

His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp Gly Met Lys
65 70 75 80
Pro Gly Ser Arg Gly Leu Ser Asp Phe Tyr
85 90

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met	Tyr	Phe	Leu	Ile	Asn	Phe	Val	Tyr	Pro	Val	Asp	Met	Val	Ile	Asn
1				5					10					15	
Leu	Pro	Phe	Leu	Ile	Asn	Thr	Gly	Leu	Ile	Val	Leu	Leu	Ser	Ala	Ile
			20					25					30		
Ser	Tyr	Ile	Ser	Leu	Leu	Val	Phe	Thr	Lys	Asp	Ser	Ile	Phe	Tyr	Glu
		35					40					45			
Phe	Leu	Asn	His	Val	Leu	Ala	Leu	Lys	Asn	Lys	Phe	Lys	Lys	Ser	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met	Arg	Val	Ile	Ala	Trp	Leu	Glu	Pro	Ser	Arg	Lys	Ile	Leu	Gln	Pro
1				5					10					15	
Gly	Ala	Asn	Asp	Val	Trp	Val	Val	Lys	Arg	Lys	Gly	Lys	Arg	Asp	Leu
			20					25					30		
Leu	Leu	Pro	Tyr	Ile	Pro	Pro	Val	Val	Leu	Asn	Val	Asp	Ile	Pro	Asn
		35					40					45			

Lys Arg Val Asp Val Glu Ile Leu Glu Gly Leu Asp Asp Glu Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Asp Asp Asp Phe Lys Arg Tyr Asn Ala Pro Ile Leu Thr Trp Tyr
 1 5 10 15
 Glu Thr Ala Arg Tyr Ala Phe Glu Arg Gly Met Val Trp Gln Asn Leu
 20 25 30
 Gly Gly Val Glu Asn Ser Leu Asn Gly Gly Leu Tyr His Phe Lys Glu
 35 40 45
 Lys Phe Asn Pro Thr Ile Glu Glu Tyr Leu Gly Glu Phe Thr Met Pro
 50 55 60
 Thr His Pro Leu Tyr Pro Leu Leu Arg Leu Ala Leu Asp Phe Arg Lys
 65 70 75 80
 Thr Leu Arg Lys Lys His Arg Lys
 85

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met Glu Asp Phe Phe Ala Trp Cys Arg Arg Gln Ser Val Leu Ser Gly
 1 5 10 15
 Ser Lys Leu Gly Arg Ala Ile Glu Tyr Ser Leu Lys Tyr Glu Glu Thr
 20 25 30

```

Phe Lys Thr Ile Leu Lys Asp Gly His Leu Val Leu Ser Asn Asn Leu
   35              40              45
Ala Glu Arg Ala Ile Lys Ser Leu Val Met Gly Arg Ser Lys Arg Val
   50              55              60
Gln Trp Thr Leu Leu Ala
   65              70

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

Met Thr Lys Gln Gly Ser Trp Lys Leu Ile Leu Glu Asp Glu Ser Ala
  1              5              10              15
Gly Arg Glu Leu Phe Pro Ile Leu Thr Gln Gly Xaa Tyr Ile Ala Thr
              20              25              30
Phe Asp Gln Gln Ala Pro Xaa Ile Asp Glu Ile Phe Lys Leu
   35              40              45

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

Met Thr Thr Asn Xaa Asp Asn Asp Thr Ser Glu Arg Ser Asp Cys Tyr
  1              5              10              15
Arg Lys Arg Thr Ala Gly Glu Thr Pro Met Asn Asp Leu Thr Ser His
              20              25              30
Thr His Gly Gly Asn Tyr Thr Ile Ala Arg Tyr Gln Glu Glu Lys Phe
   35              40              45

```


Trp Asn Lys Gln Leu
50

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Met Ala Gln His Ala Ala Val Glu Ala Leu Thr Ala Gly Lys Asn Asp
 1             5             10             15
Ala Glu Pro Met Lys Lys Glu Tyr Ile Gln Arg Arg Asp Tyr Ile Ile
          20             25             30
Glu Lys Met Thr Ala Leu Gly Phe Glu Ile Ile Lys Pro Asp Gly Ala
      35             40             45
Phe Tyr Ile Phe Ala Lys Ile Pro Ala Gly Tyr Asn Gln Asp Ser Phe
      50             55             60
Ala Phe Leu Lys Asp Phe Ala Gln Lys Lys Ala Val Ala Phe Ile Pro
65             70             75             80
Gly Ala Ala Phe Gly Arg Tyr Gly Glu Gly Tyr Val Arg Leu Ser Tyr
          85             90             95
Ala Ala Ser Met Glu Thr Ile Lys Glu Ala Met Lys Arg Leu Glu Glu
          100             105             110
Tyr Met Arg Glu Ala
          115

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp Glu Thr
 1             5             10             15
Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln Leu Gly
      20             25             30
Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val Pro Arg
      35             40             45
Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr Lys Glu
      50             55             60
Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu Ser Leu
      65             70             75             80
Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu Leu Pro
      85             90             95

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

Met Leu Gln Trp Ile Asp Arg Thr Phe Gln Asp Tyr Leu Glu Leu Glu
 1             5             10             15
His Leu Val Leu Thr Thr Trp Ser Gly Asn Leu Gly Met Met Lys Leu
      20             25             30
Ala Glu Lys Leu Xaa Met Lys Lys Xaa Ala His Ile Xaa Lys Val Arg
      35             40             45
Tyr Tyr Gln Gly Lys Tyr Phe Asp Ser Ile Lys Tyr Gly Ile Leu Arg
      50             55             60
Xaa Asp Trp Glu Lys Ile Asn Asp Gly Tyr Tyr Gln Ile Tyr Xaa Asn
      65             70             75             80
Ser

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

Met Ile Val Glu Glu Val Arg Asp Arg Tyr Val Gly Lys Val Asp Ala
 1             5             10             15
Val Phe His Asn Gly Asp Ser Glu Leu Arg Pro Asp Ser Pro Leu Trp
          20             25             30
Glu Gly Ile Arg Val Val Lys Gly Asn Met Asp Phe Tyr Ala Gly Tyr
      35             40             45
Pro Glu Arg Leu Val Thr Glu Leu Gly Ser Thr Lys Ile Ile Gln Thr
      50             55             60
His Gly His Leu Phe Asp Ile Asn Phe Asn Phe Gln Lys Leu Asp Tyr
      65             70             75             80
Trp Ala Gln Glu Glu Glu Ala Ala Ile Cys Leu Tyr Gly His Leu His
          85             90             95
Val Pro Ser Ala Trp Leu Glu Gly Lys Ile Leu Phe Leu Asn Pro Gly
          100             105             110
Ser Ile Ser Gln Pro Arg Gly Thr Ile Arg Glu Cys Leu Tyr Ala Arg
          115             120             125
Val Glu Ile Asp Asp Ser Tyr Phe Lys Val Asp Phe Leu Thr Arg Asp
          130             135             140
His Glu Val Tyr Pro Gly Cys Pro Arg Ser Leu Ala Asp Asp Ala Lys
      145             150             155             160
Glu Leu Arg Leu Ser Val Gly Ala Glu Asn Phe
          165             170

```

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

```

Met Asn Leu His Gln Pro Leu His Val Leu Pro Gly Val Gly Pro Lys
 1             5             10             15

```

Ser Ala Glu Lys Tyr Ala Lys Leu Gly Ile Glu Asn Leu Gln Asp Leu
 20 25 30
 Leu Leu Tyr Phe Pro Phe Arg Tyr Glu Asp Phe Lys Thr Lys Gln Val
 35 40 45
 Leu Glu Leu Glu Asp Gly Glu Lys Ala Val Leu Ser Gly Gln Val Val
 50 55 60
 Thr Pro Ala Ser Val Gln Tyr Tyr Gly Phe Gln Ala Ala Asn Pro Pro
 65 70 75 80
 Ala Phe Leu Val Leu Gln Ala Arg Glu Glu Gly Ser Phe Phe Phe Gly
 85 90 95
 Gly

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Gln Leu Leu Ser Glu Asn Met Leu Lys Thr Ile Gln Ser Leu Ser
 1 5 10 15
 Val Trp Gln Ile Tyr Leu Leu Gly Phe Glu Arg Ile Leu Ala Leu Gly
 20 25 30
 Phe Gln Leu Leu Leu Thr Val Trp Val Tyr Gln Ala Val Arg Gln Lys
 35 40 45
 Lys Trp Ile Tyr Leu Leu Ala Ala Tyr Gly Leu His Ala Phe Phe Asp
 50 55 60
 Leu Ala Pro Ser Leu Phe Gln Val Gly Trp Leu Thr Asn Pro Val Leu
 65 70 75 80
 Val Glu Val Ile Leu Ala Leu Glu Leu Val Leu Val Ala Tyr Gly Thr
 85 90 95
 Lys Glu Ile Phe Cys Lys Lys Ser
 100

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

Met Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
 1           5           10           15
Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
      20           25           30
Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
      35           40           45
Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
      50           55           60
Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
      65           70           75           80
Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
      85           90           95
Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
      100          105          110
Thr His Ile Leu Gln Glu Val Glu Ile Met
      115          120

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

Met Leu Asn Ser Ile Val Thr Ile Ile Cys Ile Ala Leu Ile Ala Phe
 1           5           10           15
Ile Leu Phe Trp Phe Phe Lys Lys Pro Glu Lys Ser Gly Gln Lys Ala
      20           25           30
Gln Gln Lys Asn Gly Tyr Gln Glu Ile Arg Val Glu Val Met Gly Gly
      35           40           45

```

```

Tyr Thr Pro Glu Leu Ile Val Leu Lys Lys Ser Val Pro Ala Arg Ile
 50                      55                      60
Val Phe Asp Arg Lys Asp Pro Ser Pro Cys Leu Asp Gln Ile Val Phe
 65                      70                      75                      80
Pro Asp Phe Gly Val His Ala Asn Leu Pro Met Gly Glu Glu Tyr Val
                      85                      90                      95
Val Glu Ile Thr Pro Glu Gln Ala Gly Glu Phe Gly Phe Ala Cys Gly
                      100                      105                      110
Met Asn Met Met His Gly Lys Met Ile Val Glu
                      115                      120

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
 1                      5                      10                      15
Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
                      20                      25                      30
Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Xaa Val Leu Asp Leu
                      35                      40                      45
Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
                      50                      55                      60
Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Val
 65                      70                      75                      80
Ala Glu Asn Ile Gln Met Thr Lys Glu Val Gly Lys Phe Gln Leu Leu
                      85                      90                      95
Gln Asn Gly Cys Arg Lys Gly Ile Gly Thr Gly Xaa Leu Gly Asn Leu
                      100                      105                      110
Thr Ser Phe Ser
                      115

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

Met Xaa Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
 1             5             10             15
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
      20             25             30
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
      35             40             45
Val Asn Leu Val
      50

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

Met Ile Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His
 1             5             10             15
Leu Thr His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg
      20             25             30
Leu Phe Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser
      35             40             45
Val Val Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys
      50             55             60
Thr Ala Gln Lys Ser Ile His Cys His Ala Arg
      65             70             75

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
 1             5             10             15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
             20             25             30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
             35             40             45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
             50             55             60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
65             70             75             80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly Gly His Ile
             85             90             95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
             100            105            110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
             115            120            125
Leu Trp
             130

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

Met Thr Phe Ile Arg Gly Pro Ile Ile Ser Thr Val Gly Glu Gly Val
 1             5             10             15
Xaa Ile Leu Ala Thr Val Asn Xaa Gln Phe Val Xaa Xaa Gln Xaa Xaa
             20             25             30

```


Asn Met Leu Val Ser Pro Phe His Pro Glu Leu Thr Asp Xaa Xaa Arg
 35 40 45
 Leu Xaa Gln Tyr Phe Ile Ser Met Cys Lys Glu Lys Ser Xaa Asp
 50 55 60

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
 1 5 10 15
 Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
 20 25 30
 Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asp Lys Ala Leu Ala Asp Leu Lys Thr Ser Gly His Leu Pro Ile
 1 5 10 15
 Pro Arg His Leu Arg Asp Gly His Tyr Xaa Gly Ser Lys Glu Leu Gly
 20 25 30
 Asn Ala Gln Asp Tyr Leu Tyr Pro His Asn Tyr Pro Xaa Asn Trp Val
 35 40 45
 Lys Gln Asp Tyr Leu Pro Gln Lys Ile Arg Asn His His Tyr Phe Gln
 50 55 60

(2) INFORMATION FOR SEQ ID NO:455:

(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

(2) INFORMATION FOR SEQ ID NO:456:

(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

332

```

Ala Tyr His Asp Glu Glu Trp Gly Gln Pro Leu His Asp Asp Gln Ala
      20                      25                      30
Leu Phe Glu Leu Leu Cys Met Glu Thr Tyr Gln Ala Gly Leu Ser Trp
      35                      40                      45
Glu Thr Val Leu Asn Lys Arg Gln Ala Phe Arg Glu Ala Phe Pro
      50                      55                      60

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

Met Phe Val Gly Gln Glu Trp Thr Asn Gln Thr Phe Val Asp Leu Leu
  1                      5                      10                      15
Gly Asn His Gln Gly Gln Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln
      20                      25                      30
Phe Pro Val Ser Ala Arg Ser Val Ser Val Trp Ala Val Asn Thr Ile
      35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

Met Ala Gln Val Asp Ile Ile His Gly Ile Gly Thr Gly Val Ile Arg
  1                      5                      10                      15
Glu Gly Val Thr Lys Tyr Leu Gln Arg Asn Lys His Val Lys Ser Phe
      20                      25                      30
Gly Tyr Ala Pro Gln Asn Ala Gly Gly Ser Gly Ala Thr Ile Val Thr
      35                      40                      45

```

Phe Lys Gly
50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met	Asn	Leu	Leu	Glu	Glu	Ala	Thr	Lys	Gly	Lys	Val	Ile	Phe	Glu	Gly
1				5					10					15	
Val	Asp	Ile	Thr	Asp	Lys	Lys	Asn	Asp	Leu	Phe	Pro	Met	Arg	Glu	Lys
			20					25					30		
Met	Gly	Met	Val	Phe	Gln	Gln	Phe	Asn	Xaa	Phe	Leu	Ile			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met	Gln	Ile	Asp	Leu	Ala	Asn	Leu	Leu	Pro	Asp	Leu	Pro	Gly	Asn	Leu
1				5					10				15		
Ser	Gly	Ile	Asn	Pro	Asn	Arg	Tyr	Val	Phe	Tyr	Gln	Asp	Val	Leu	Cys
			20					25				30			
Pro	Ile	Leu	Asp	Arg	His	Met	Thr	Pro	Glu	Gln	Asp	Lys	Pro	His	Phe
		35					40					45			
Ala	Gln	Ala	Ala	Gly	Thr	Ile	Ala	Asp	Ile	Lys	Glu	Lys	Ala	Gly	Asn
	50					55				60					
Tyr	Ala	Tyr	Leu	Phe	Glu	Thr	Gln	Ala	Gln	Leu	Asn	Ala	Ile	Leu	Ser
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:461:

(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

(2) INFORMATION FOR SEQ ID NO:462:

(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

335

```

Phe Leu Leu Val Met Asp Asn Ala Ile Trp His Lys Ser Ser Val Leu
      20                      25                      30
Lys Ile Pro Thr Asn Ile Gly Phe Ala Phe Ile Pro Pro Tyr Thr Pro
      35                      40                      45
Glu Met Asn Pro Ile Glu Gln Val Trp Lys Glu Ile Arg Lys Arg Gly
      50                      55                      60
Phe Lys Asn Lys Ala Phe Arg Ile Leu Glu Asp Val Met Asn Gln Leu
      65                      70                      75                      80
Gln Asp Val Ile Gln Gly Leu Glu Lys Glu Val Ile Lys Ser Ile Val
      85                      90                      95
Asn Arg Arg Trp Thr Arg Met Leu Phe Glu Ser Arg
      100                      105

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```

Met Thr Val Glu Glu Glu Lys Val Phe Leu Ala Arg His Leu Lys Ala
  1                      5                      10                      15
Thr Glu Ala Gly Glu Phe Val Thr Ile Asp Ala Leu Phe Gln Ala Tyr
      20                      25                      30
Lys Lys Glu Leu Gly Arg Ser Tyr Thr Arg Asp Ala Phe Tyr Gln Leu
      35                      40                      45
Leu Lys Arg His Gly Trp Arg Asn Ile Met Pro Arg Pro Glu His Pro
      50                      55                      60
Lys Lys Ala Asp Ala Gln Thr Ile Val Ala Ser Lys Asn Lys Ile Ser
      65                      70                      75                      80
Ile Gln Glu Asp Lys Lys Ala Ile
      85

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear °

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

Met Leu Ser Leu Val Val Leu Ile Thr Gln Tyr Ala Thr His Gly Glu
 1             5             10             15
Leu Phe Glu Asn Tyr Ile Ser Lys Glu Asn Asp Asn Val Ile Lys Glu
          20             25             30
Tyr Gln Asn Thr Thr Gly Phe Ser Thr Pro Tyr Thr Leu Asp Gly Ser
      35             40             45
Val Leu Ile Val His Pro Asp Leu Thr Lys Gly Met Asn Ile Glu Gly
      50             55             60
Tyr Ser Asp Leu Leu Lys Pro Glu Leu Lys Gly Lys Ile Ala Thr Ala
      65             70             75             80
Asp Pro Ala Asn Ser Ser Ser Ala Phe Ala Gln Leu Thr Asn Met Leu
          85             90             95
Gln Ala Gln Gly Gly Tyr Lys Asp Asp Leu Ala Trp Ser Val Leu Ser
      100             105             110
Thr Ile Phe Ser Thr Leu Ile Asp Gly Ile Val Lys
      115             120

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

```

Met Leu Ala Arg Lys Asp Arg Phe Tyr Tyr Ile Asp Lys Ala Thr Gly
 1             5             10             15
Lys Ala Leu Gly Ile Phe Leu Ser Cys Val Leu Thr Ser Asn Gly Val
          20             25             30
Ile Glu Val Gly Ala Val Thr Phe Ser Pro Lys Leu Arg Gly Thr Arg
      35             40             45

```

Ile Gly Thr Glu Ala Gln Tyr Leu Leu Ala Arg Tyr Val Phe Glu Glu
 50 55 60
 Leu Asn Tyr Arg Arg Tyr Glu Trp Lys Cys Asp Ala Leu Asn Leu Pro
 65 70 75 80
 Ser Arg Arg Ala Ala Glu Arg Leu Gly Phe Ile Tyr Glu Gly Thr Phe
 85 90 95
 Arg Gln Ala Val Val Tyr Lys Gly Arg Thr Arg Asp Met Asp Trp Leu
 100 105 110
 Ser Met Ile Asp Lys Asp Trp Pro Lys Val Lys Asp Arg Leu Glu Thr
 115 120 125
 Trp Leu Arg Pro Glu Asn Phe Asp Lys Asn Gly Gln Gln Tyr Lys Ser
 130 135 140
 Leu Arg Glu Leu
 145

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Met Thr Ser Asp Phe Phe Glu Val Trp Phe Gln Lys Phe Leu Leu
 1 5 10 15
 Pro Thr Leu Thr Thr Pro Ser Val Ile Ile Val Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:


```

Met Val Ser Thr Lys Thr Gln Ile Ala Gly Phe Glu Phe Asp Asn Cys
 1             5             10             15
Leu Met Asn Ala Ala Gly Val Ala Cys Met Thr Ile Glu Glu Leu Glu
             20             25             30
Glu Val Lys Asn Ser Ala Ala Gly Thr Phe Val Thr Lys Thr Ala Thr
             35             40             45
Leu Asp Phe Arg Gln Gly Asn Pro Glu Pro Arg Tyr Gln Asp Val Pro
             50             55             60
Leu Gly Ser Ile Asn Ser Met Gly Leu Pro Asn Asn Gly Leu Asp Tyr
65             70             75             80
Tyr Leu Asp Tyr Leu Leu Asp Leu Gln Glu Lys Glu Ser Asn Arg Thr
             85             90             95
Phe Phe Leu Ser Leu Val Gly Met Ser Pro Glu Lys Pro Ile Leu Phe
             100             105             110

```

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```

Met Thr Tyr Leu Met Phe Ser Gly Leu Asp Glu Asn Phe Tyr His Phe
 1             5             10             15
Pro Trp Glu Val Phe Ala Gly Phe Gly Ile Ile Phe Leu Ala Cys Pro
             20             25             30
Glu Lys Val
             35

```

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

Met Phe Thr Gly Trp Phe Ala Gln Thr Phe Leu His Gln Phe Ile Arg
 1           5           10           15
Gly Ala Trp Gly Leu Gly Phe Met Ile Phe Ile Ala Phe Pro Met Gly
           20           25           30
Lys Glu Leu Leu Glu Gly Glu Tyr His Glu His Asp
      35           40

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

Met Gln Glu Lys Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
 1           5           10           15
His Thr Val Ile Glu Leu Ile Gln Ala Gly His Gln Val Val Val Val
           20           25           30
Asp Asn Leu Val Asn Ser Asn Xaa Lys Ser Leu Glu Val Val Glu Arg
      35           40           45
Ile Thr Gly Val Glu Ile Pro Phe Tyr Glu Ala Asp Ile Xaa Asp Thr
      50           55           60
Asp Thr Leu Arg Asp Ile Phe Lys Gln Glu Glu Leu Thr Gly Val Ile
      65           70           75           80
His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Thr Arg Ile Pro Leu
           85           90           95
Ala Tyr Tyr Asp Asn Asn Ile Ala Gly Thr Val Ser Leu Leu Lys Ala
           100          105          110
Met Glu Glu Asn Asn Cys Lys Asn Ile Ile Phe Ser Ser Xaa Ala Thr
           115          120          125
Val Tyr Gly Asp Pro Tyr Thr Val Pro Ile Leu Glu Val Ser His Phe
      130          135          140
Gln
145

```

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Met Val Lys Glu Lys Val Thr Leu Thr Pro Leu Ala Ser Gly Tyr Gln
 1             5             10             15
Ile Gly Glu Glu Glu Phe Glu Gln Val Ile Leu Ala Xaa Gly Ala Trp
      20             25             30
Leu Gly Asp Met Leu Glu Pro Leu Gly Tyr Glu Val Asp Val Arg Pro
      35             40             45
Gln Lys Gly Gln Leu Arg Asp Tyr Gln Leu Val Gln Asp Met Glu Ala
      50             55             60
Tyr Pro Val Val Met Pro Glu Gly Glu Trp Asp Leu Ile Pro Phe Ala
65             70             75             80
Gly Gly Lys Leu Ser Leu Gly Ala Thr His Glu Asn Asp Met Gly Phe
      85             90             95
Asp Leu Thr Val Asp Glu Thr Leu Leu Gln Gln Met Glu Glu Ala Thr
      100            105            110
Leu Thr His Tyr Leu Ile Leu Ala Glu Ala Thr Ser Lys Ser Glu Arg
      115            120            125
Val Gly Ile Arg Ala Tyr Thr Ser Asp Phe Ser Pro Phe Phe Gly Gln
      130            135            140
Val Pro Asp Leu Thr Gly Val Tyr Ala Ala Ser Gly Leu Gly Ser Ser
145            150            155            160
Gly Leu Thr Thr Gly Pro Ile Ile Gly Tyr His Leu Ala Gln Leu Ile
      165            170            175
Gln Asp Lys Glu Leu Thr Leu Asp Pro Glu Asn Tyr Pro Ile Glu Asn
      180            185            190
Tyr Val Lys Arg Val Lys Ser Glu
      195            200

```

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

```

Met Glu His Ile Ile Tyr Gln Phe Glu Glu Asp Leu Ala Ile Leu Thr
 1           5           10           15
Leu Asn Arg Pro Glu Val Ala Asn Gly Phe His Ile Pro Met Cys Glu
          20           25           30
Glu Ile Leu Glu Ala Leu Thr Leu Ala Glu Glu Asn Pro Ala Val His
          35           40           45
Phe Ile Leu Ile Asn Ala Asn Gly Lys Val Phe Ser Val Gly Gly Asp
          50           55           60
Leu Val Glu Met Lys Arg Ala Val Asp Glu Asp Asp Ile Pro Ser Leu
65           70           75           80
Thr Lys Ile Ala Glu Leu Val Asn Thr Ile Ser Tyr Lys Ile Lys Gln
          85           90           95
Ile Ala Lys Pro Val Phe Asn Gly Ser
          100          105

```

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

```

Met Gln Pro Glu Val Ile Trp Leu Gln Lys Ile Ala Lys Pro Ser Gln
 1           5           10           15
Met Lys Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp
          20           25           30
Val Asp Ile Ile Gln Asn Ser Leu Gln Ile Ile Asn Gln Gln Lys Glu
          35           40           45
Leu Ile Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu
          50           55           60
Glu Lys Asp Ile Gln Thr Arg Thr Ser Cys Asp Lys Arg Asn Ala Gly
65           70           75           80
Asn

```

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

```

Met Gly Ser Asn Ser Leu Thr Leu Leu Leu Lys Ile Gln Ala Thr Ile
 1             5             10             15
Pro Arg Asn Ile Tyr Asp Asn Leu Gln Ala Gly Ser Lys Val Thr Leu
      20             25             30
Asp Arg Ala Tyr Gly His Met Ile Ile Glu Glu Gly Arg Glu Asn Gln
      35             40             45
Val Trp Ile Ala Gly Gly Ile Gly Ile Thr Pro Phe Ile Ser Tyr Ile
      50             55             60
Arg Glu His Pro Ile Leu Asp Lys Gln Val His Phe Tyr Tyr Ser Phe
      65             70             75             80
Arg Gly Asp Glu Asn Ala Val Tyr Leu Asp Leu Leu Arg Asn Tyr Ala
      85             90             95
Gln Lys Asn Pro Asn Phe Glu Leu His Leu Ile Asp Ser Thr Lys Asp
      100            105            110
Gly Tyr Leu Asn Phe Glu Gln Lys Lys Cys Pro Asn Met Gln Pro Ser
      115            120            125
Ile Cys Val Val Leu Phe Leu
      130            135

```

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

```

Met Phe Phe Val Leu Ala Tyr Ala Lys Ala Val Ala Gly Arg Asn Ile
 1           5           10           15
Lys Leu His Pro Ile Gln Arg Gln Gly Ala Gly Tyr His Ser Val Asn
      20           25           30
Lys Asp Val Asp Phe Ala Ser Ala Thr Ala Leu Arg Gln His Gln Lys
      35           40           45
Asp Gln Asp Phe Leu Glu Arg Phe Met Pro Ser Val Ala Leu Phe Glu
      50           55           60
Gln Ala Ser Lys Val Ile Trp Glu Asp Tyr Phe Pro Leu Leu Arg Tyr
65           70           75           80
Gln Ile Leu Ser Asn Pro Asp Leu Thr Thr Ile Tyr Gln Val Asn Gln
      85           90           95
Glu Met Ala Val Arg Ile Lys Glu Ala Ile Lys Thr Ala Gln Ser Val
      100          105          110
Glu Glu Leu Val Glu Leu Val Thr Thr Lys Arg Tyr Thr Lys Ala Arg
      115          120          125
Val Arg Arg Leu Leu Thr Tyr Ile Leu Met Gln Ala Arg Glu Ser Asp
      130          135          140
Leu Pro Glu Ala Ile His Val Leu Gly Phe Thr Glu Lys Gly Arg Gln
145          150          155          160
His Leu Lys Ser Leu Lys Gly Gln Val Asn Leu Val Ser Arg Ile Gly
      165          170          175
Lys Glu Pro Trp Asp Ala Met Thr Gln Lys Val Asp Gln Ile Tyr Gln
      180          185          190
Leu Gly Lys Pro Ser Ile Ala Glu Gln Asn Phe Gly Arg Val Pro Ile
      195          200          205
Arg Ile Glu Thr Asn
      210

```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

Met Leu Gly Ser Met Phe Val Gly Leu Leu Val Gly Phe Leu Ala Gly
 1           5           10           15

```

Ala Met Thr Asn Arg Gly Glu Arg Met Gly Cys Phe Gly Lys Met Phe
 20 25 30
 Leu Gly Trp Ile Gly Ala Phe Leu Gly His Leu Leu Phe Gly Thr Trp
 35 40 45
 Gly Pro Val Leu Ser Gly Thr Ala Ile Ile Pro Ala Val Leu Gly Ala
 50 55 60
 Met Ile Val Leu Ala Ile Phe Trp Arg Arg Gly Ser
 65 70 75

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Arg Ser Ser Pro Ser Arg Glu Ile Gln Pro Arg Ser Trp Gly Ile
 1 5 10 15
 Thr Thr Val Tyr Val Thr His Asp Gln Glu Gly Ala Met Ala Ile Ser
 20 25 30
 Asp Gln Ile Ala Cys Tyr Glu Arg Trp Gly Asp Pro Thr Asn Arg Pro
 35 40 45
 Thr Lys Arg Thr Val Ser
 50

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:224 through 477,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the
10 same mature polypeptide expressed by the a gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
- 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.
5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from
20 the group consisting of SEQ ID NO:1 through 223.
6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
7. A vector comprising the polynucleotide of Claim 1.
8. A host cell comprising the vector of Claim 7.
- 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
10. A process for producing a novel polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
- 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:224 through 477.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
 - (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:
 - contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;
 - and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/or T cell immune response to protect said animal from disease.

21. An isolated Streptococcal polypeptide having one of the amino acid sequences of SEQ ID NO:224 through SEQ ID NO:234.
22. An isolated nucleic acid encoding one of the amino acid sequences of Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent
5 conditions.
23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.
24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds
10 capable of inhibiting the bioactivity of said polypeptide.
25. Antimicrobial compounds identified by the method of Claim 24.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P --- Y, P	WO 96/10647 A1 (FUSO PHARMACEUTICAL INDUSTRIES, LTD.) 11 April 1996, claim 2, pages 22-24.	1, 2, 7, 8, and 22 ----- 3, 6, 9-12, 15, 17, 21, and 23-25
Y	WATSON, J. D. et al. Recombinant DNA, Second Edition. New York: Scientific American Books, W.H. Freeman and Company, 1992, pages 73 and 74, see entire document.	1-3, 6-12, 15, 17, and 21-23
Y	KENNEL, D. E. Principles and Practices of Nucleic Acid Hybridization. Progress in Nucleic Acid Research Molecular Biology. 1971, Vol. 11, pages 259-301, see especially pages 259-262.	1-3, 6-12, 15, 17, and 21-23

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	* "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
* "A" document defining the general state of the art which is not considered to be of particular relevance	* "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
* "E" earlier document published on or after the international filing date	* "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
* "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* "A" document member of the same patent family
* "O" document referring to an oral disclosure, use, exhibition or other means	
* "P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

10 JULY 1997

Date of mailing of the international search report

06 AUG 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3, 6-12, 15, 17, and 21-23 (SEQ ID NOs 224-233).

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I. Claims 1-12, 15, 17, and 21-23, drawn to nucleic acids and polypeptides of specific sequence, vectors containing nucleic acids, methods of producing polypeptides, and methods of treatment using polypeptides.

Group II. Claims 13 and 19, drawn to antibodies against any of no fewer than 254 specific sequence polypeptides.

Group III. Claims 14 and 16, drawn to antagonists of undisclosed composition of the activity of no fewer than 254 specific sequence polypeptides.

Group IV. Claims 18 and 24, drawn to methods for screening for compounds that interact with no fewer than 254 specific sequence polypeptides.

Group V. Claim 20, drawn to a method of inducing an immunological response using a nucleic acid.

Group VI. Claim 25, drawn to compounds of undisclosed composition.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons. The nucleic acids, proteins, and methods of Group I are materially different from the antibodies of Group II, the compounds of Group III, and the compounds of Group VI and are not required to produce either the antibodies of Group II, which antibodies may be made with antigens other than those embraced by Group I. Additionally, the methods of Group I are not needed to produce the compounds of either one of Groups III or VI. The compositions and methods of Group I are not needed for the methods of either one of Groups IV or V. The antibodies of Group II are not needed for the methods of Groups IV or V and are materially different from the compounds of Groups III and VI. The antagonists of Group III are materially different from the compounds of Group VI because the antagonists and compounds have differing sites of action and/or binding. Neither are the compounds of either one of Groups III or VI needed to practice the methods of either one of Groups IV or V. The methods of Groups IV and V may be practiced independently of one another.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows. Each of the 234 SEQ ID NOs listed is a separate species because there is no relationship between the species.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons. There is no relationship among the species.

For any Group applicant elects, a total of 10 (TEN) specified sequences will be searched and no more than 4 (FOUR) specified sequences will be searched for each additional fee paid.

The claims are deemed to correspond to the species listed above in the following manner: SEQ ID NOs 224-233 correspond to claims 1-3, 6-12, 15, 17, and 21-23.

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 15/31, 15/11, 15/00; C12P 21/02; A61K 38/16, 39/09; C07K 14/195, 14/315

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MPSRCH OF: A-GENESEQ26, A-ISSUED, HIV-AA8, PIR50, SUIWW-PROT34, EMBL-NEW11, GENBANK97, GENBANK-NEW11, U-EMBL48_97, HIV-NA8, N-GENESEQ26, N-ISSUED, EST-STS, EST-STS-TWO, EST-STS-

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

THREE. SEQ ID NOs 224-233.